Figure 1: 254P1D6B SSH sequence of 186 nucleotides (SEQ ID NO: 1).

```
  1 GATCCACAGA TAGGACACAA TTCTTTGGTC ATCAGTAGAC CTTGAACCAT CCAAAGTAAT
 61 GGAATTATTG GGAAGCACAA GAACATGTCT GCCACCAGCC CGGGCTCTGG GAGGACTATT
121 ATTTTCCTTC TTCACAGCCA CAGTGAGGGT GGACGTGCTG CTCAGTCCCT GCTGGTCTTT
181 TACTGTCAAA CGGAAGTGGT AGGTCCCCAC CTGGAGACCA GTCACAGTGG CTATTGCTTT
241 GTCAATATTT TCCATCTCCA CTGCACTGGG GCCTCTGACG TGCT
```

Figure 2:

Figure 2A. The cDNA (SEQ ID NO. : 2) and amino acid sequence (SEQ ID NO. : 3) of 254P1D6B v.1 clone LCP-3. The start methionine is underlined. The open reading frame extends from nucleic acid 512-3730 including the stop codon.

```
   1 gctgccgcgggcggtgggcggggatcccccgggggtgcaaccttgctccacctgtgctgc
  61 cctcggcgggcctggctggccccgcgcagagcggcggcggcgctcgctgtcactgccgga
 121 ggtgagagcgcagcagtagcttcagcctgtcttgggcttggtccagattcgctcctctgg
 181 ggctacgtcccggggaagaggaagcgaggattttgctggggtggggctgtacctcttaac
 241 agcaggtgcgcgcgcgagggtgtgaacgtgtgtgtgtgtgtgtgtstgtgtgtgtgtgg
 301 taagacctgcgatgacgacgaggaggaacaagtgggacggcgagtgatgctcagggccag
 361 cagcaacgcatggggcgagcttcagtgtcgccagcagtgaccacagttcttgaggccaaa
 421 tctggctcctaaaaaacatcaaaggaagcttgcaccaaactctcttcagggccgcctcag
   1                                   M  A  P  P  T  G  V  L  S  S
 481 aagcctgccatcacccactgtgtggtgcacaATGGCGCCCCCCACAGGTGTGCTCTCTTC
  11  L  L  L  L  V  T  I  A  G  C  A  R  K  Q  C  S  E  G  R  T
 541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCGTAAGCAGTGCAGCGAGGGGAGGAC
  31  Y  S  N  A  V  I  S  P  N  L  E  T  T  R  I  M  R  V  S  H
 601 ATATTCCAATGCAGTCATTTCACCTAACTTGGAAACCACCAGAATCATGCGGGTGTCTCA
  51  T  F  P  V  V  D  C  T  A  A  C  C  D  L  S  S  C  D  L  A
 661 CACCTTCCCTGTCGTAGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
  71  W  W  F  E  G  R  C  Y  L  V  S  C  P  H  K  E  N  C  E  P
 721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAAGAGAACTGTGAGCC
  91  K  K  M  G  P  I  R  S  Y  L  T  F  V  L  R  P  V  Q  R  P
 781 CAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCTGTTCAGAGGCC
 111  A  Q  L  L  D  Y  G  D  M  M  L  N  R  G  S  P  S  G  I  W
 841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCCCCCTCGGGGATCTG
 131  G  D  S  P  E  D  I  R  K  D  L  P  F  L  G  K  D  W  G  L
 901 GGGGGACTCACCTGAGGATATCAGAAAGGACTTGMCCTTTCTAGGCAAAGATTGGGGCCT
 151  E  E  M  S  E  Y  S  D  D  Y  R  E  L  E  K  D  L  L  Q  P
 961 AGAGGAGATGTCTGAGTACKCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
 171  S  G  K  Q  E  P  R  G  S  A  E  Y  T  D  W  G  L  L  P  G
1021 CAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG
 191  S  E  G  A  F  N  S  S  V  G  D  S  P  A  V  P  A  E  T  Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCTGCGGTGCCAGCGGAGACGCA
 211  Q  D  P  E  L  H  Y  L  N  E  S  A  S  T  P  A  P  K  L  P
1141 GCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCCAAAACTCCC
 231  E  R  S  V  L  L  P  L  P  T  T  P  S  S  G  E  V  L  E  K
1201 TGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
 251  E  K  A  S  Q  L  Q  E  Q  S  S  N  S  S  G  K  E  V  L  M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
 271  P  S  H  S  L  P  P  A  S  L  E  L  S  S  V  T  V  E  K  S
1321 GCCTTCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
```

291 P V L T V T P G S T E H S I P T P P T S

1381 CCCAGTGCTCACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCACTAG

311 A A P S E S T P S E L P I S P T T A P R

1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCACTGCTCCCAG

331 T V K E L T V S A G D N L I I T L P D N

1501 GACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA

351 E V E L K A F V A P A P P V E T T Y N Y

1561 TGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAACTA

371 E W N L I S H P T D Y Q G E I K Q G H K

1621 TGAATGGAATTTAATAAGCCACCCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA

391 Q T L N L S Q L S V G L Y V F K V T V S

1681 GCAAACTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC

411 S E N A F G E G F V N V T V K P A R R V

1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT

431 N L P P V A V V S P Q L Q E L T L P L T

1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC

451 S A L I D G S Q S T D D T E I V S Y H W

1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG

471 E E I N G P F I E E K T S V D S P V L R

1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG

491 L S N L D P G N Y S F R L T V T D S D G

1981 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTTACAGACTCGGACGG

511 A T N S T T A A L I V N N A V D Y P P V

2041 AGCCACTAACTCTACAACTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCAGT

531 A N A G P N H T I T L P Q N S I T L N G

2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACTCCATCACTTTGAATGG

551 N Q S S D D H Q I V L Y E W S L G P G S

2161 AAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAGTGGTCCCTGGGTCCTGGGAG

571 E G K H V V M Q G V Q T P Y L H L S A M

2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT

591 Q E G D Y T F Q L K V T D S S R Q Q S T

2281 GCAGGAAGGAGATTATACATTTCAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC

611 A V V T V I V Q P E N N R P P V A V A G

2341 TGCTGTRGTGACTGTGATTGTCCAGCCTGAAAACAATAGACCTCCAGTGGCTGTGGCCGG

631 P D K E L I F P V E S A T L D G S S S S

2401 CCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACCCTGGATGGGAGCAGCAGCAG

651 D D H G I V F Y H W E H V R G P S A V E

2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTCAGAGGCCCCAGTGCAGTGGA

671 M E N I D K A I A T V T G L Q V G T Y H

2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA

691 F R L T V K D Q Q G L S S T S T L T V A

2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCACGTCCACCCTCACTGTGGC

711 V K K E N N S P P R A R A G G R H V L V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCCAGAGCCCGGGCTGGTGGCAGACATGTTCTTGT
731 L P N N S I T L D G S R S T D D Q R I V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
751 S Y L W I R D G Q S P A A G D V I D G S
2761 GTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
771 D H S V A L Q L T N L V E G V Y T F H L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCCACTT
791 R V T D S Q G A S D T D T A T V E V Q P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
811 D P R K S G L V E L T L Q V G V G Q L T
2941 AGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAGGTTGGTGTTGGGCAGCTGAC
831 E Q R K D T L V R Q L A V L L N V L D S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
851 D I K V Q K I R A H S D L S T V I V F Y
3061 GGACATTAAGGTCCAGAAGATTCGGGCCCACTCGGATCTCAGCACCGTGATTGTGTTTTA
871 V Q S R P P F K V L K A A E V A R N L H
3121 TGTACAGAGCAGGCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCGAAATCTGCA
891 M R L S K E K A D F L L F K V L R V D T
3181 CATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTCTTGAGGGTTGATAC
911 A G C L L K C S G H G H C D P L T K R C
3241 AGCAGGTTGCCTTCTGAAGTGTTCTGGCCATGGTCACTGCGACCCCCTCACAAAGCGCTG
931 I C S H L W M E N L I Q R Y I W D G E S
3301 CATTTGCTCTCACTTATGGATGGAGAACCTTATACAGCGTTATATCTGGGATGGAGAGAG
951 N C E W S I F Y V T V L A F T L I V L T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTTGGCTTTTACTCTTATTGTGCTAAC
971 G G F T W L C I C C C K R Q K R T K I R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAAGGACTAAAATCAG
991 K K T K Y T I L D N M D E Q E R M E L R
3481 GAAAAAAACAAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAACTGAG
1011 P K Y G I K H R S T E H N S S L M V S E
3541 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAACTCCAGCCTGATGGTATCCGA
1031 S E F D S D Q D T I F S R E K M E R G N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051 P K V S M N G S I R N G A S F S Y C S K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCCTTCAGTTATTGCTCAAA
1071 D R *
3721 GGACAGATAAtggcgcagttcattgtaaagtggaaggacccyttgaatccargaccagtc
3781 agtgggagttacagcacaaaacccactcttttagaatagttcattgaccttcttccccag
3841 tgggttagatgtgtatccccacgtactaaaagaccggtttttgaaggcacaaaacaaaaa
3901 ctttgctcttttaactgagatgcttgttaatagaaataaaggctgggtaaaactytaagg
3961 tatatacttaaaagagttttgagtttttgtagctggcacaatctcatattaaagatgaac

4021 aacgatttctatctgtagaaccttagagaaggtgaatgaaacaaggttttaaaaagggat
4081 gatttctgtcttagcygctgtgattgcctctaaggaacagcattctaaacacggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgttaaaatagcttgtctaagaggcacggg
4201 ccatctgtggaggtacggagtcttgcatgtagcaagctttctgtgctgacggcaacactc
4261 gcacagtgccaagccctcctggtttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttggccattcaagagctaaggaagaatcgtattctaaggact
4381 gaggcaatagaaaggggaggaggagcttaatgccrtgcaggttgaaggtagcattgtaac
4441 attatcttttctttctctaagaaaaactacactgactcctctcggtgttgtttagcagta
4501 tagttctctaatgtaaacrgatccccagtttacattaartgcaatagaagtgattaattc
4561 attaagcatttattatgttctgtaggctgtgcgtttggactgccatagataggkataacg
4621 actcagcaattgtgtatatattccaaaactctgaaatacagtcagtcttaacttggatgg
4681 cgtggttatgatactctggtccccgacaggtactttccaaaataacttgacatagatgta
4741 ttcacttcatatgtttaaaaatacatttaagtttttctaccgaataaatcttatttcaaa
4801 catgaaagacaattaaaacattcccacccacaaagcagtactcccgagcaattaactgga
4861 gttaattgtagcctgctacgttgactggttcagggtagttccccatccacccttggtcct
4921 gaggctggtggccttggtggtgcccttggcatttttgtgggaagattagaatgagagat
4981 agaaccagtgttgtggtaccaagtgtgagcacacctaaacaatatcctgttgcacaatgc
5041 ttttttaacacatgggaaaactaggaatgcattgctgatgaagaagcaaggtatttaaac
5101 accagggcaggagtgccagagaaaatgtttccccatgggttcttaaaaaaaattcagctt
5161 ttaggtgcttttgtcatctcccgsagtattcatcctcatgggaccatcttatttttactt
5221 attgtaatttactggggaaaggcagaactaaaaagtgtgtcattttatttttaaaataat
5281 tgctttgcttatgcctacactttctgtataactagccaattcaatactgtctatagtgtt
5341 agaaggaaaatgtgatttttttttttttaaccagtattgagcttcataagcctagaatctg
5401 ccttatcaggtgaccagggttatggttgtttgcatgcaaatgtgaatttctggcatagggg
5461 gacagcagcccaaatgtaaagtcatcgggcgtaatgaggaagaagggagtgaacatttac
5521 cgctttakgtacataacatatgcagtttacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattcttatgttgcagatagccctctgaaggcccagagaggttaa
5641 rtaacttcccagaggtcatggccaagaagtagtggctccaagaactgaatgcaaattttt
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc
5761 aaattctggtggaacttttgggccacctgaaagttctattcccaggactaagaggaattt
5821 cttttaatggatccagagagccaaggtcagagggagagatggcctgcatagtctcctgtg
5881 gatcacacccgggccacccctccctctaggtttacagtggacttcttctgcccctcctcc
5941 ttttctgtccttggccatctcagcctggcctctctgatccttccatcacagaaggatctt
6001 gaatctctgggaaatcaaacatcacagtagtgatcagaaagtgagtcctgtcttgtcacc
6061 ccatttctcatcagaacaaagcacgagatggaatgaccaaccagcattcttcatggtgga
6121 ctgcttatcattgaggatctttgggagataaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtgggtgtttgtagggctcayargctaacaagcactttag
6241 ttgctggtttacattcaatgaaggaggattcatacccatggcattacaaggctaagcatg
6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccacctttgtgcgcggggaggagagtgactaccattgtttttgtgt
6421 gacaaagctatcatggactattttaatcttggttttattgcttaaaatatattatttttc
6481 cctatgtgttgacaaggtatttctaatatcacactattaaatatatgcactaatctaaat

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6541 aaaggtgtctgtattttctgtaatgcttatttttaggggaaatttgttttctttatgct
6601 tcagggtagagggattcccttgagtataggtcagcaaactctggcctgcagcctgtgtgt
6661 gcacgccccatgagccgaaaagtgggtcttatgttttcaaatggttaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattcagatttgtgttcataaataaagttttatt
6781 ggaacatatcc
```

Figure 2B. The cDNA (SEQ ID NO. : 4) and amino acid sequence (SEQ ID NO. : 5) of 254P1D6B v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 512-3730 including the stop codon.

```
   1 gctgccgcgggcggtgggcggggatcccccgggggtgcaaccttgctccacctgtgctgc
  61 cctcggcgggcctggctggccccgcgcagagcggcggcggcgctcgctgtcactgccgga
 121 ggtgagagcgcagcagtagcttcagcctgtcttgggcttggtccagattcgctcctctgg
 181 ggctacgtcccggggaagaggaagcgaggattttgctggggtggggctgtacctcttaac
 241 agcaggtgcgcgcgcgagggtgtgaacgtgtgtgtgtgtgtgtgtctgtgtgtgtgtg
 301 taagacctgcgatgacgacgaggaggaacaagtgggacggcgagtgatgctcagggccag
 361 cagcaacgcatggggcgagcttcagtgtcgccagcagtgaccacagttcttgaggccaaa
 421 tctggctcctaaaaaacatcaaaggaagcttgcaccaaactctcttcagggccgcctcag
   1                                   M  A  P  P  T  G  V  L  S  S
 481 aagcctgccatcacccactgtgtggtgcacaATGGCGCCCCCCACAGGTGTGCTCTCTTC
  11  L  L  L  L  V  T  I  A  G  C  A  R  K  Q  C  S  E  G  R  T
 541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCGTAAGCAGTGCAGCGAGGGGAGGAC
  31  Y  S  N  A  V  I  S  P  N  L  E  T  T  R  I  M  R  V  S  H
 601 ATATTCCAATGCAGTCATTTCACCTAACTTGGAAACCACCAGAATCATGCGGGTGTCTCA
  51  T  F  P  V  V  D  C  T  A  A  C  C  D  L  S  S  C  D  L  A
 661 CACCTTCCCTGTCGTAGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
  71  W  W  F  E  G  R  C  Y  L  V  S  C  P  H  K  E  N  C  E  P
 721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAAGAGAACTGTGAGCC
  91  K  K  M  G  P  I  R  S  Y  L  T  F  V  L  R  P  V  Q  R  P
 781 CAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCTGTTCAGAGGCC
 111  A  Q  L  L  D  Y  G  D  M  M  L  N  R  G  S  P  S  G  I  W
 841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCCCCCTCGGGGATCTG
 131  G  D  S  P  E  D  I  R  K  D  L  P  F  L  G  K  D  W  G  L
 901 GGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTTCTAGGCAAAGATTGGGGCCT
 151  E  E  M  S  E  Y  A  D  D  Y  R  E  L  E  K  D  L  L  Q  P
 961 AGAGGAGATGTCTGAGTACGCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
 171  S  G  K  Q  E  P  R  G  S  A  E  Y  T  D  W  G  L  L  P  G
1021 CAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG
 191  S  E  G  A  F  N  S  S  V  G  D  S  P  A  V  P  A  E  T  Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCTGCGGTGCCAGCGGAGACGCA
 211  Q  D  P  E  L  H  Y  L  N  E  S  A  S  T  P  A  P  K  L  P
1141 GCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCCAAAACTCCC
 231  E  R  S  V  L  L  P  L  P  T  T  P  S  S  G  E  V  L  E  K
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1201 TGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
 251  E  K  A  S  Q  L  Q  E  Q  S  S  N  S  S  G  K  E  V  L  M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
 271  P  S  H  S  L  P  P  A  S  L  E  L  S  S  V  T  V  E  K  S
1321 GCCTTCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
 291  P  V  L  T  V  T  P  G  S  T  E  H  S  I  P  T  P  P  T  S
1381 CCCAGTGCTCACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCACTAG
 311  A  A  P  S  E  S  T  P  S  E  L  P  I  S  P  T  T  A  P  R
1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCACTGCTCCCAG
 331  T  V  K  E  L  T  V  S  A  G  D  N  L  I  I  T  L  P  D  N
1501 GACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA
 351  E  V  E  L  K  A  F  V  A  P  A  P  P  V  E  T  T  Y  N  Y
1561 TGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAACTA
 371  E  W  N  L  I  S  H  P  T  D  Y  Q  G  E  I  K  Q  G  H  K
1621 TGAATGGAATTTAATAAGCCACCCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA
 391  Q  T  L  N  L  S  Q  L  S  V  G  L  Y  V  F  K  V  T  V  S
1681 GCAAACTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC
 411  S  E  N  A  F  G  E  G  F  V  N  V  T  V  K  P  A  R  R  V
1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT
 431  N  L  P  P  V  A  V  V  S  P  Q  L  Q  E  L  T  L  P  L  T
1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC
 451  S  A  L  I  D  G  S  Q  S  T  D  D  T  E  I  V  S  Y  H  W
1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG
 471  E  E  I  N  G  P  F  I  E  E  K  T  S  V  D  S  P  V  L  R
1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG
 491  L  S  N  L  D  P  G  N  Y  S  F  R  L  T  V  T  D  S  D  G
1981 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTTACAGACTCGGACGG
 511  A  T  N  S  T  T  A  A  L  I  V  N  N  A  V  D  Y  P  P  V
2041 AGCCACTAACTCTACAACTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCAGT
 531  A  N  A  G  P  N  H  T  I  T  L  P  Q  N  S  I  T  L  N  G
2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACTCCATCACTTTGAATGG
 551  N  Q  S  S  D  D  H  Q  I  V  L  Y  E  W  S  L  G  P  G  S
2161 AAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAGTGGTCCCTGGGTCCTGGGAG
 571  E  G  K  H  V  V  M  Q  G  V  Q  T  P  Y  L  H  L  S  A  M
2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT
 591  Q  E  G  D  Y  T  F  Q  L  K  V  T  D  S  S  R  Q  Q  S  T
2281 GCAGGAAGGAGATTATACATTTCAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC
 611  A  V  V  T  V  I  V  Q  P  E  N  N  R  P  P  V  A  V  A  G
2341 TGCTGTAGTGACTGTGATTGTCCAGCCTGAAAACAATAGACCTCCAGTGGCTGTGGCCGG
 631  P  D  K  E  L  I  F  P  V  E  S  A  T  L  D  G  S  S  S  S
2401 CCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACCCTGGATGGGAGCAGCAGCAG
 651  D  D  H  G  I  V  F  Y  H  W  E  H  V  R  G  P  S  A  V  E
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2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTCAGAGGCCCCAGTGCAGTGGA
 671  M  E  N  I  D  K  A  I  A  T  V  T  G  L  Q  V  G  T  Y  H
2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA
 691  F  R  L  T  V  K  D  Q  Q  G  L  S  S  T  S  T  L  T  V  A
2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCACGTCCACCCTCACTGTGGC
 711  V  K  K  E  N  N  S  P  P  R  A  R  A  G  G  R  H  V  L  V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCCAGAGCCCGGGCTGGTGGCAGACATGTTCTTGT
 731  L  P  N  N  S  I  T  L  D  G  S  R  S  T  D  D  Q  R  I  V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
 751  S  Y  L  W  I  R  D  G  Q  S  P  A  A  G  D  V  I  D  G  S
2761 GTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
 771  D  H  S  V  A  L  Q  L  T  N  L  V  E  G  V  Y  T  F  H  L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCCACTT
 791  R  V  T  D  S  Q  G  A  S  D  T  D  T  A  T  V  E  V  Q  P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
 811  D  P  R  K  S  G  L  V  E  L  T  L  Q  V  G  V  G  Q  L  T
2941 AGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAGGTTGGTGTTGGGCAGCTGAC
 831  E  Q  R  K  D  T  L  V  R  Q  L  A  V  L  L  N  V  L  D  S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
 851  D  I  K  V  Q  K  I  R  A  H  S  D  L  S  T  V  I  V  F  Y
3061 GGACATTAAGGTCCAGAAGATTCGGGCCCACTCGGATCTCAGCACCGTGATTGTGTTTTA
 871  V  Q  S  R  P  P  F  K  V  L  K  A  A  E  V  A  R  N  L  H
3121 TGTACAGAGCAGGCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCGAAATCTGCA
 891  M  R  L  S  K  E  K  A  D  F  L  L  F  K  V  L  R  V  D  T
3181 CATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTCTTGAGGGTTGATAC
 911  A  G  C  L  L  K  C  S  G  H  G  H  C  D  P  L  T  K  R  C
3241 AGCAGGTTGCCTTCTGAAGTGTTCTGGCCATGGTCACTGCGACCCCCTCACAAAGCGCTG
 931  I  C  S  H  L  W  M  E  N  L  I  Q  R  Y  I  W  D  G  E  S
3301 CATTTGCTCTCACTTATGGATGGAGAACCTTATACAGCGTTATATCTGGGATGGAGAGAG
 951  N  C  E  W  S  I  F  Y  V  T  V  L  A  F  T  L  I  V  L  T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTTGGCTTTTACTCTTATTGTGCTAAC
 971  G  G  F  T  W  L  C  I  C  C  C  K  R  Q  K  R  T  K  I  R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAAGGACTAAAATCAG
 991  K  K  T  K  Y  T  I  L  D  N  M  D  E  Q  E  R  M  E  L  R
3481 GAAAAAAACAAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAACTGAG
1011  P  K  Y  G  I  K  H  R  S  T  E  H  N  S  S  L  M  V  S  E
3541 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAACTCCAGCCTGATGGTATCCGA
1031  S  E  F  D  S  D  Q  D  T  I  F  S  R  E  K  M  E  R  G  N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051  P  K  V  S  M  N  G  S  I  R  N  G  A  S  F  S  Y  C  S  K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCCTTCAGTTATTGCTCAAA
1071  D  R  *
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3721 GGACAGATAAtggcgcagttcattgtaaagtggaaggacccccttgaatccaagaccagtc
3781 agtgggagttacagcacaaaacccactcttttagaatagttcattgaccttcttccccag
3841 tgggttagatgtgtatccccacgtactaaaagaccggtttttgaaggcacaaaacaaaaa
3901 ctttgctcttttaactgagatgcttgttaatagaaataaaggctgggtaaaactctaagg
3961 tatatacttaaaagagttttgagtttttgtagctggcacaatctcatattaaagatgaac
4021 aacgatttctatctgtagaaccttagagaaggtgaatgaaacaaggttttaaaaagggat
4081 gatttctgtcttagccgctgtgattgcctctaaggaacagcattctaaacacggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgttaaaatagcttgtctaagaggcacggg
4201 ccatctgtggaggtacggagtcttgcatgtagcaagctttctgtgctgacggcaacactc
4261 gcacagtgccaagccctcctggtttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttggccattcaagagctaaggaagaatcgtattctaaggact
4381 gaggcaatagaaaggggaggaggagcttaatgccgtgcaggttgaaggtagcattgtaac
4441 attatcttttctttctctaagaaaaactacactgactcctctcggtgttgtttagcagta
4501 tagttctctaatgtaaacggatccccagtttacattaaatgcaatagaagtgattaattc
4561 attaagcatttattatgttctgtaggctgtgcgtttggactgccatagatagggataacg
4621 actcagcaattgtgtatatattccaaaactctgaaatacagtcagtcttaacttggatgg
4681 cgtggttatgatactctggtccccgacaggtactttccaaaataacttgacatagatgta
4741 ttcacttcatatgtttaaaaatacatttaagtttttctaccgaataaatcttatttcaaa
4801 catgaaagacaattaaaacattcccacccacaaagcagtactcccgagcaattaactgga
4861 gttaattgtagcctgctacgttgactggttcagggtagttccccatccacccttggtcct
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5161 ttaggtgcttttgtcatctcccggagtattcatcctcatgggaccatcttatttttactt
5221 attgtaatttactggggaaaggcagaactaaaaagtgtgtcatttttatttttaaaataat
5281 tgctttgcttatgcctacactttctgtataactagccaattcaatactgtctatagtgtt
5341 agaaggaaaatgtgatttttttttttttaaccagtattgagcttcataagcctagaatctg
5401 ccttatcaggtgaccagggttatggttgtttgcatgcaaatgtgaatttctggcataggg
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5521 cgctttatgtacataacatatgcagtttacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattcttatgttgcagatagccctctgaaggcccagagaggttaa
5641 gtaacttcccagaggtcatggccaagaagtagtggctccaagaactgaatgcaaattttt
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc
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5821 cttttaatggatccagagagccaaggtcagagggagagatggcctgcatagtctcctgtg
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6061 ccatttctcatcagaacaaagcacgagatggaatgaccaaccagcattcttcatggtgga
6121 ctgcttatcattgaggatctttgggagataaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtgggtgtttgtagggctcataggctaacaagcactttag

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6241 ttgctggtttacattcaatgaaggaggattcatacccatggcattacaaggctaagcatg
6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccacctttgtgcgcggggaggagagtgactaccattgttttttgtgt
6421 gacaaagctatcatggactattttaatcttggttttattgcttaaaatatattatttttc
6481 cctatgtgttgacaaggtatttctaatatcacactattaaatatatgcactaatctaaat
6541 aaaggtgtctgtattttctgtaatgcttatttttaggggggaaatttgttttctttatgct
6601 tcagggtagagggattcccttgagtataggtcagcaaactctggcctgcagcctgtgtgt
6661 gcacgccccatgagccgaaaagtgggtcttatgttttcaaatggttaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattcagatttgtgttcataaataaagttttatt
6781 ggaacatatcc
```

Figure 2C. The cDNA (SEQ ID NO. : 6) and amino acid sequence (SEQ ID NO. : 7) of 254P1D6B v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 739-3930 including the stop codon.

```
   1 gctgccgcgggcggtgggcggggatcccccgggggtgcaaccttgctccacctgtgctgc
  61 cctcggcgggcctggctggccccgcgcagagcggcggcggcgctcgctgtcactgccgga
 121 ggtgagagcgcagcagtagcttcagcctgtcttgggcttggtccagattcgctcctctgg
 181 ggctacgtcccggggaagaggaagcgaggattttgctggggtggggctgtacctcttaac
 241 agcaggtgcgcgcgcgagggtgtgaacgtgtgtgtgtgtgtgtgtctgtgtgtgtgtg
 301 taagacctgcgatgacgacgaggaggaacaagtgggacggcgagtgatgctcagggccag
 361 cagcaacgcatggggcgagcttcagtgtcgccagcagtgaccacaggtacggtatctact
 421 tcccagagcgcctggccgagaaataggaaagagggcagccagtaggcaggccaatаccca
 481 acaaaagtagaatcgagacgccctgagttcagaagttcttgaggccaaatctggctccta
 541 aaaaacatcaaaggaagcttgcaccaaactctcttcagggccgcctcagaagcctgccat
 601 cacccactgtgtggtgcacaatggcgccccccacaggtgtgctctcttcattgctgctgc
 661 tggtgacaattgcagtttgcttatggtggatgcactcatggcaaaaaaatcactggtgag
   1                   M  T  R  L  G  W  P  S  P  C  C  A  R  K
 721 catcatttaagaagacccATGACTAGACTGGGCTGGCCGAGCCCATGTTGTGCCCGTAAG
  15 Q  C  S  E  G  R  T  Y  S  N  A  V  I  S  P  N  L  E  T  T
 781 CAGTGCAGCGAGGGGAGGACATATTCCAATGCAGTCATTTCACCTAACTTGGAAACCACC
  35 R  I  M  R  V  S  H  T  F  P  V  V  D  C  T  A  A  C  C  D
 841 AGAATCATGCGGGTGTCTCACACCTTCCCTGTCGTAGACTGCACGGCCGCTTGCTGTGAC
  55 L  S  S  C  D  L  A  W  W  F  E  G  R  C  Y  L  V  S  C  P
 901 CTGTCCAGCTGTGACCTGGCCTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCC
  75 H  K  E  N  C  E  P  K  K  M  G  P  I  R  S  Y  L  T  F  V
 961 CACAAAGAGAACTGTGAGCCCAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTG
  95 L  R  P  V  Q  R  P  A  Q  L  L  D  Y  G  D  M  M  L  N  R
1021 CTCCGGCCTGTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGG
 115 G  S  P  S  G  I  W  G  D  S  P  E  D  I  R  K  D  L  P  F
1081 GGCTCCCCCTCGGGGATCTGGGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTT
 135 L  G  K  D  W  G  L  E  E  M  S  E  Y  S  D  D  Y  R  E  L
1141 CTAGGCAAAGATTGGGGCCTAGAGGAGATGTCTGAGTACTCAGATGACTACCGGGAGCTG
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 155 E  K  D  L  L  Q  P  S  G  K  Q  E  P  R  G  S  A  E  Y  T
1201 GAGAAGGACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACG
 175 D  W  G  L  L  P  G  S  E  G  A  F  N  S  S  V  G  D  S  P
1261 GACTGGGGCCTACTGCCGGGCAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCT
 195 A  V  P  A  E  T  Q  Q  D  P  E  L  H  Y  L  N  E  S  A  S
1321 GCGGTGCCAGCGGAGACGCAGCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCA
 215 T  P  A  P  K  L  P  E  R  S  V  L  L  P  L  P  T  T  P  S
1381 ACCCCTGCCCCAAAACTCCCTGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCT
 235 S  G  E  V  L  E  K  E  K  A  S  Q  L  Q  E  Q  S  S  N  S
1441 TCAGGAGAGGTGTTGGAGAAAGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGC
 255 S  G  K  E  V  L  M  P  S  H  S  L  P  P  A  S  L  E  L  S
1501 TCTGGAAAAGAGGTTCTAATGCCTTCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGC
 275 S  V  T  V  E  K  S  P  V  L  T  V  T  P  G  S  T  E  H  S
1561 TCAGTCACCGTGGAGAAAAGCCCAGTGCTCACAGTCACCCCGGGGAGTACAGAGCACAGC
 295 I  P  T  P  P  T  S  A  A  P  S  E  S  T  P  S  E  L  P  I
1621 ATCCCAACACCTCCCACTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATA
 315 S  P  T  T  A  P  R  T  V  K  E  L  T  V  S  A  G  D  N  L
1681 TCTCCTACCACTGCTCCCAGGACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTA
 335 I  I  T  L  P  D  N  E  V  E  L  K  A  F  V  A  P  A  P  P
1741 ATTATAACTTTACCCGACAATGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCT
 355 V  E  T  T  Y  N  Y  E  W  N  L  I  S  H  P  T  D  Y  Q  G
1801 GTAGAAACAACCTACAACTATGAATGGAATTTAATAAGCCACCCCACAGACTACCAAGGT
 375 E  I  K  Q  G  H  K  Q  T  L  N  L  S  Q  L  S  V  G  L  Y
1861 GAAATAAAACAAGGACACAAGCAAACTCTTAACCTCTCTCAATTGTCCGTCGGACTTTAT
 395 V  F  K  V  T  V  S  S  E  N  A  F  G  E  G  F  V  N  V  T
1921 GTCTTCAAAGTCACTGTTTCTAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACT
 415 V  K  P  A  R  R  V  N  L  P  P  V  A  V  V  S  P  Q  L  Q
1981 GTTAAGCCTGCCAGAAGAGTCAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAA
 435 E  L  T  L  P  L  T  S  A  L  I  D  G  S  Q  S  T  D  D  T
2041 GAGCTCACTTTGCCTTTGACGTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACT
 455 E  I  V  S  Y  H  W  E  E  I  N  G  P  F  I  E  E  K  T  S
2101 GAAATAGTGAGTTATCATTGGGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCA
 475 V  D  S  P  V  L  R  L  S  N  L  D  P  G  N  Y  S  F  R  L
2161 GTTGACTCTCCCGTCTTACGCTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTG
 495 T  V  T  D  S  D  G  A  T  N  S  T  T  A  A  L  I  V  N  N
2221 ACTGTTACAGACTCGGACGGAGCCACTAACTCTACAACTGCAGCCCTAATAGTGAACAAT
 515 A  V  D  Y  P  P  V  A  N  A  G  P  N  H  T  I  T  L  P  Q
2281 GCTGTGGACTACCCACCAGTTGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAA
 535 N  S  I  T  L  N  G  N  Q  S  S  D  D  H  Q  I  V  L  Y  E
2341 AACTCCATCACTTTGAATGGAAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAG
 555 W  S  L  G  P  G  S  E  G  K  H  V  V  M  Q  G  V  Q  T  P
2401 TGGTCCCTGGGTCCTGGGAGTGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCA
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 575 Y  L  H  L  S  A  M  Q  E  G  D  Y  T  F  Q  L  K  V  T  D
2461 TACCTTCATTTATCTGCAATGCAGGAAGGAGATTATACATTTCAGCTGAAGGTGACAGAT
 595 S  S  R  Q  Q  S  T  A  V  V  T  V  I  V  Q  P  E  N  N  R
2521 TCTTCAAGGCAACAGTCTACTGCTGTGGTGACTGTGATTGTCCAGCCTGAAAACAATAGA
 615 P  P  V  A  V  A  G  P  D  K  E  L  I  F  P  V  E  S  A  T
2581 CCTCCAGTGGCTGTGGCCGGCCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACC
 635 L  D  G  S  S  S  S  D  D  H  G  I  V  F  Y  H  W  E  H  V
2641 CTGGATGGGAGCAGCAGCAGCGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTC
 655 R  G  P  S  A  V  E  M  E  N  I  D  K  A  I  A  T  V  T  G
2701 AGAGGCCCCAGTGCAGTGGAGATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGT
 675 L  Q  V  G  T  Y  H  F  R  L  T  V  K  D  Q  Q  G  L  S  S
2761 CTCCAGGTGGGGACCTACCACTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGC
 695 T  S  T  L  T  V  A  V  K  K  E  N  N  S  P  P  R  A  R  A
2821 ACGTCCACCCTCACTGTGGCTGTGAAGAAGGAAAATAATAGTCCTCCCAGAGCCCGGGCT
 715 G  G  R  H  V  L  V  L  P  N  N  S  I  T  L  D  G  S  R  S
2881 GGTGGCAGACATGTTCTTGTGCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCT
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2941 ACTGATGACCAAAGAATTGTGTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCT
 755 G  D  V  I  D  G  S  D  H  S  V  A  L  Q  L  T  N  L  V  E
3001 GGAGATGTCATCGATGGCTCTGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAG
 775 G  V  Y  T  F  H  L  R  V  T  D  S  Q  G  A  S  D  T  D  T
3061 GGGGTGTACACTTTCCACTTGCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACT
 795 A  T  V  E  V  Q  P  D  P  R  K  S  G  L  V  E  L  T  L  Q
3121 GCCACTGTGGAAGTGCAGCCAGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAG
 815 V  G  V  G  Q  L  T  E  Q  R  K  D  T  L  V  R  Q  L  A  V
3181 GTTGGTGTTGGGCAGCTGACAGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTG
 835 L  L  N  V  L  D  S  D  I  K  V  Q  K  I  R  A  H  S  D  L
3241 CTGCTGAACGTGCTGGACTCGGACATTAAGGTCCAGAAGATTCGGGCCCACTCGGATCTC
 855 S  T  V  I  V  F  Y  V  Q  S  R  P  P  F  K  V  L  K  A  A
3301 AGCACCGTGATTGTGTTTTATGTACAGAGCAGGCCGCCTTTCAAGGTTCTCAAAGCTGCT
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3361 GAAGTGGCCCGAAATCTGCACATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTC
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3421 AAGGTCTTGAGGGTTGATACAGCAGGTTGCCTTCTGAAGTGTTCTGGCCATGGTCACTGC
 915 D  P  L  T  K  R  C  I  C  S  H  L  W  M  E  N  L  I  Q  R
3481 GACCCCCTCACAAAGCGCTGCATTTGCTCTCACTTATGGATGGAGAACCTTATACAGCGT
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3601 TTTACTCTTATTGTGCTAACAGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGA
 975 Q  K  R  T  K  I  R  K  K  T  K  Y  T  I  L  D  N  M  D  E
3661 CAAAAAAGGACTAAAATCAGGAAAAAAACAAAGTACACCATCCTGGATAACATGGATGAA
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 995 Q  E  R  M  E  L  R  P  K  Y  G  I  K  H  R  S  T  E  H  N
3721 CAGGAAAGAATGGAACTGAGGCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAAC
1015 S  S  L  M  V  S  E  S  E  F  D  S  D  Q  D  T  I  F  S  R
3781 TCCAGCCTGATGGTATCCGAGTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGA
1035 E  K  M  E  R  G  N  P  K  V  S  M  N  G  S  I  R  N  G  A
3841 GAAAAGATGGAGAGAGGGAATCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCT
1055 S  F  S  Y  C  S  K  D  R  *
3901 TCCTTCAGTTATTGCTCAAAGGACAGATAAtggcgcagttcattgtaaagtggaaggacc
3961 ccttgaatccaagaccagtcagtgggagttacagcacaaaacccactcttttagaatagt
4021 tcattgaccttcttccccagtgggttagatgtgtatccccacgtactaaaagaccggttt
4081 ttgaaggcacaaaacaaaaactttgctcttttaactgagatgcttgttaatagaaataaa
4141 ggctgggtaaaactctaaggtatatacttaaaagagttttgagtttttgtagctggcaca
4201 atctcatattaaagatgaacaacgatttctatctgtagaaccttagagaaggtgaatgaa
4261 acaaggttttaaaaagggatgatttctgtcttagccgctgtgattgcctctaaggaacag
4321 cattctaaacacggtttctcttgtaggacctgcagtcagatggctgtgtatgttaaaata
4381 gcttgtctaagaggcacgggccatctgtggaggtacggagtcttgcatgtagcaagcttt
4441 ctgtgctgacggcaacactcgcacagtgccaagccctcctggtttttaattctgtgctat
4501 gtcaatggcagttttcatctctctcaagaaagcagctgttggccattcaagagctaagga
4561 agaatcgtattctaaggactgaggcaatagaaaggggaggaggagcttaatgccgtgcag
4621 gttgaaggtagcattgtaacattatcttttctttctctaagaaaaactacactgactcct
4681 ctcggtgttgtttagcagtatagttctctaatgtaaacggatccccagtttacattaaat
4741 gcaatagaagtgattaattcattaagcatttattatgttctgtaggctgtgcgtttggac
4801 tgccatagatagggataacgactcagcaattgtgtatatattccaaaactctgaaataca
4861 gtcagtcttaacttggatggcgtggttatgatactctggtccccgacaggtactttccaa
4921 aataacttgacatagatgtattcacttcatatgtttaaaaatacatttaagtttttctac
4981 cgaataaatcttatttcaaacatgaaagacaattaaaacattcccacccacaaagcagta
5041 ctcccgagcaattaactggagttaattgtagcctgctacgttgactggttcagggtagtt
5101 ccccatccacccttggtcctgaggctggtggccttggtggtgcccttggcatttttgtg
5161 ggaagattagaatgagagatagaaccagtgttgtggtaccaagtgtgagcacacctaaac
5221 aatatcctgttgcacaatgctttttaacacatgggaaaactaggaatgcattgctgatg
5281 aagaagcaaggtatttaaacaccagggcaggagtgccagagaaaatgtttccccatgggt
5341 tcttaaaaaaaattcagcttttaggtgcttttgtcatctcccggagtattcatcctcatg
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5461 cattttatttttaaaataattgctttgcttatgcctacactttctgtataactagccaat
5521 tcaatactgtctatagtgttagaaggaaaatgtgatttttttttttttaaccagtattgag
5581 cttcataagcctagaatctgccttatcaggtgaccagggttatggttgtttgcatgcaaa
5641 tgtgaatttctggcataggggacagcagcccaaatgtaaagtcatcgggcgtaatgagga
5701 agaagggagtgaacatttaccgctttatgtacataacatatgcagtttacatactcattt
5761 gatccttataatcaaccttgaagaggagatactatcattcttatgttgcagatagccctc
5821 tgaaggcccagagaggttaagtaacttcccagaggtcatggccaagaagtagtggctcca
5881 agaactgaatgcaaatttttaaactgtagagttctgctttccactaaacaaagaactcc
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6121 acttcttctgcccctcctccttttctgtccttggccatctcagcctggcctctctgatcc
6181 ttccatcacagaaggatcttgaatctctgggaaatcaaacatcacagtagtgatcagaaa
6241 gtgagtcctgtcttgtcaccccatttctcatcagaacaaagcacgagatggaatgaccaa
6301 ccagcattcttcatggtggactgcttatcattgaggatctttgggagataaagcacgcta
6361 agagctctggacagagaaaaacaggccctagaatatgggagtgggtgtttgtagggctca
6421 taggctaacaagcactttagttgctggtttacattcaatgaaggaggattcatacccatg
6481 gcattacaaggctaagcatgtgtatgactaaggaactatctgaaaaacatgcagcaaggt
6541 aagaaaatgtaccactcaacaagccagtgatgccacctttgtgcgcggggaggagagtg
6601 actaccattgtttttgtgtgacaaagctatcatggactattttaatcttggttttattg
6661 cttaaaatatattatttttccctatgtgttgacaaggtatttctaatatcacactattaa
6721 atatatgcactaatctaaataaaggtgtctgtattttctgtaatgcttatttttaggggg
6781 aaatttgttttctttatgcttcagggtagagggattcccttgagtataggtcagcaaact
6841 ctggcctgcagcctgtgtgtgcacgccccatgagccgaaaagtgggtcttatgttttcaa
6901 atggttaaaaataaataaaaaaatttgaaacatgtgaactatatgacattcagatttgtg
6961 ttcataaataaagttttattggaacatatcc

Figure 2D. 254P1D6B v.4 through v.20, SNP variants of 254P1D6B v.1. The 254P1D6B v.4 through v.20 proteins have 1072 amino acids. Variants 254P1D6B v.4 through v.20 are variants with single nucleotide difference from 254P1D6B v.1. 254P1D6B v.5 and v.6 proteins differ from 254P1D6B v.1 by one amino acid. 254P1D6B v.4 and v.7 through v.20 proteins code for the same protein as v.1. Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above in Figures 2A, Figure 2B and Figure 2C.

Variant	Nucleic acid position	Nucleic Acid Variation	Amino Acid Position	Amino Acid Variation
254P1D6B v.4	286	C/G	*Silent variant*	
254P1D6B v.5	935	C/A	142	P=>T
254P1D6B v.6 (Identical AA as v.2)	980	T/G	157	S=>A
254P1D6B v.7	2347	G/A	*Silent variant*	
254P1D6B v.8	3762	C/T	*Silent variant*	
254P1D6B v.9	3772	A/G	*Silent variant*	
254P1D6B v.10	3955	C/T	*Silent variant*	
254P1D6B v.11	4096	C/T	*Silent variant*	
254P1D6B v.12	4415	G/A	*Silent variant*	
254P1D6B v.13	4519	G/A	*Silent variant*	
254P1D6B v.14	4539	A/G	*Silent variant*	

Variant	Nucleic acid position	Nucleic Acid Variation	Amino Acid Position	Amino Acid Variation
254P1D6B v.15	4614	G/T	*Silent variant*	
254P1D6B v.16	5184	G/C	*Silent variant*	
254P1D6B v.17	5528	T/G	*Silent variant*	
254P1D6B v.18	5641	G/A	*Silent variant*	
254P1D6B v.19	6221	T/C	*Silent variant*	
254P1D6B v.20	6223	G/A	*Silent variant*	

Figure 3:

Figure 3A. Amino acid sequence 254P1D6B v.1 clone LCP-3 (SEQ ID NO. : 8). The 254P1D6B v.1 clone LCP-3 protein has 1072 amino acids.

```
   1 MAPPTGVLSS LLLLVTIAGC ARKQCSEGRT YSNAVISPNL ETTRIMRVSH TFPVVDCTAA
  61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPIRSYL TFVLRPVQRP AQLLDYGDMM
 121 LNRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYSDDY RELEKDLLQP SGKQEPRGSA
 181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
 241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
 301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLPDN EVELKAFVAP
 361 APPVETTYNY EWNLISHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
 421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
 481 KTSVDSPVLR LSNLDPGNYS FRLTVTDSDG ATNSTTAALI VNNAVDYPPV ANAGPNHTIT
 541 LPQNSITLNG NQSSDDHQIV LYEWSLGPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
 601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
 661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
 721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
 781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
 841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF
 901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
 961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KKTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSDQDTI FSREKMERGN PKVSMNGSIR NGASFSYCSK DR
```

Figure 3B. Amino acid sequence 254P1D6B v.2 (SEQ ID NO.: 9). The 254P1D6B v.2 protein has 1072 amino acids.

```
   1 MAPPTGVLSS LLLLVTIAGC ARKQCSEGRT YSNAVISPNL ETTRIMRVSH TFPVVDCTAA
  61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPIRSYL TFVLRPVQRP AQLLDYGDMM
 121 LNRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYADDY RELEKDLLQP SGKQEPRGSA
 181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
 241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
 301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLPDN EVELKAFVAP
 361 APPVETTYNY EWNLISHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
 421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
 481 KTSVDSPVLR LSNLDPGNYS FRLTVTDSDG ATNSTTAALI VNNAVDYPPV ANAGPNHTIT
 541 LPQNSITLNG NQSSDDHQIV LYEWSLGPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
 601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
 661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
 721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
 781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
 841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF
 901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
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961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KKTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSDQDTI FSREKMERGN PKVSMNGSIR NGASFSYCSK DR

Figure 3C. Amino acid sequence 254P1D6B v.3 (SEQ ID NO: 10). The 254P1D6B v.3 protein has 1063 amino acids.

1 MTRLGWPSPC CARKQCSEGR TYSNAVISPN LETTRIMRVS HTFPVVDCTA ACCDLSSCDL
61 AWWFEGRCYL VSCPHKENCE PKKMGPIRSY LTFVLRPVQR PAQLLDYGDM MLNRGSPSGI
121 WGDSPEDIRK DLPFLGKDWG LEEMSEYSDD YRELEKDLLQ PSGKQEPRGS AEYTDWGLLP
181 GSEGAFNSSV GDSPAVPAET QQDPELHYLN ESASTPAPKL PERSVLLPLP TTPSSGEVLE
241 KEKASQLQEQ SSNSSGKEVL MPSHSLPPAS LELSSVTVEK SPVLTVTPGS TEHSIPTPPT
301 SAAPSESTPS ELPISPTTAP RTVKELTVSA GDNLIITLPD NEVELKAFVA PAPPVETTYN
361 YEWNLISHPT DYQGEIKQGH KQTLNLSQLS VGLYVFKVTV SSENAFGEGF VNVTVKPARR
421 VNLPPVAVVS PQLQELTLPL TSALIDGSQS TDDTEIVSYH WEEINGPFIE EKTSVDSPVL
481 RLSNLDPGNY SFRLTVTDSD GATNSTTAAL IVNNAVDYPP VANAGPNHTI TLPQNSITLN
541 GNQSSDDHQI VLYEWSLGPG SEGKHVVMQG VQTPYLHLSA MQEGDYTFQL KVTDSSRQQS
601 TAVVTVIVQP ENNRPPVAVA GPDKELIFPV ESATLDGSSS SDDHGIVFYH WEHVRGPSAV
661 EMENIDKAIA TVTGLQVGTY HFRLTVKDQQ GLSSTSTLTV AVKKENNSPP RARAGGRHVL
721 VLPNNSITLD GSRSTDDQRI VSYLWIRDGQ SPAAGDVIDG SDHSVALQLT NLVEGVYTFH
781 LRVTDSQGAS DTDTATVEVQ PDPRKSGLVE LTLQVGVGQL TEQRKDTLVR QLAVLLNVLD
841 SDIKVQKIRA HSDLSTVIVF YVQSRPPFKV LKAAEVARNL HMRLSKEKAD FLLFKVLRVD
901 TAGCLLKCSG HGHCDPLTKR CICSHLWMEN LIQRYIWDGE SNCEWSIFYV TVLAFTLIVL
961 TGGFTWLCIC CCKRQKRTKI RKKTKYTILD NMDEQERMEL RPKYGIKHRS TEHNSSLMVS
1021 ESEFDSDQDT IFSREKMERG NPKVSMNGSI RNGASFSYCS KDR

Figure 3D. Amino acid sequence 254P1D6B v.5 (SEQ ID NO: 11). The 254P1D6B v.5 protein has 1072 amino acids.

1 MAPPTGVLSS LLLLVTIAGC ARKQCSEGRT YSNAVISPNL ETTRIMRVSH TFPVVDCTAA
61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPIRSYL TFVLRPVQRP AQLLDYGDMM
121 LNRGSPSGIW GDSPEDIRKD LTFLGKDWGL EEMSEYSDDY RELEKDLLQP SGKQEPRGSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLPDN EVELKAFVAP
361 APPVETTYNY EWNLISHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
481 KTSVDSPVLR LSNLDPGNYS FRLTVTDSDG ATNSTTAALI VNNAVDYPPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT

961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KKTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSDQDTI FSREKMERGN PKVSMNGSIR NGASFSYCSK DR

Figure 3E. Amino acid sequence 254P1D6B v.6 (SEQ ID NO: 12). The 254P1D6B v.6 protein has 1072 amino acids.

1 MAPPTGVLSS LLLLVTIAGC ARKQCSEGRT YSNAVISPNL ETTRIMRVSH TFPVVDCTAA
61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPIRSYL TFVLRPVQRP AQLLDYGDMM
121 LNRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYADDY RELEKDLLQP SGKQEPRGSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLPDN EVELKAFVAP
361 APPVETTYNY EWNLISHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
481 KTSVDSPVLR LSNLDPGNYS FRLTVTDSDG ATNSTTAALI VNNAVDYPPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KKTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSDQDTI FSREKMERGN PKVSMNGSIR NGASFSYCSK DR

Figure 5: 254P1D6B variant 1
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

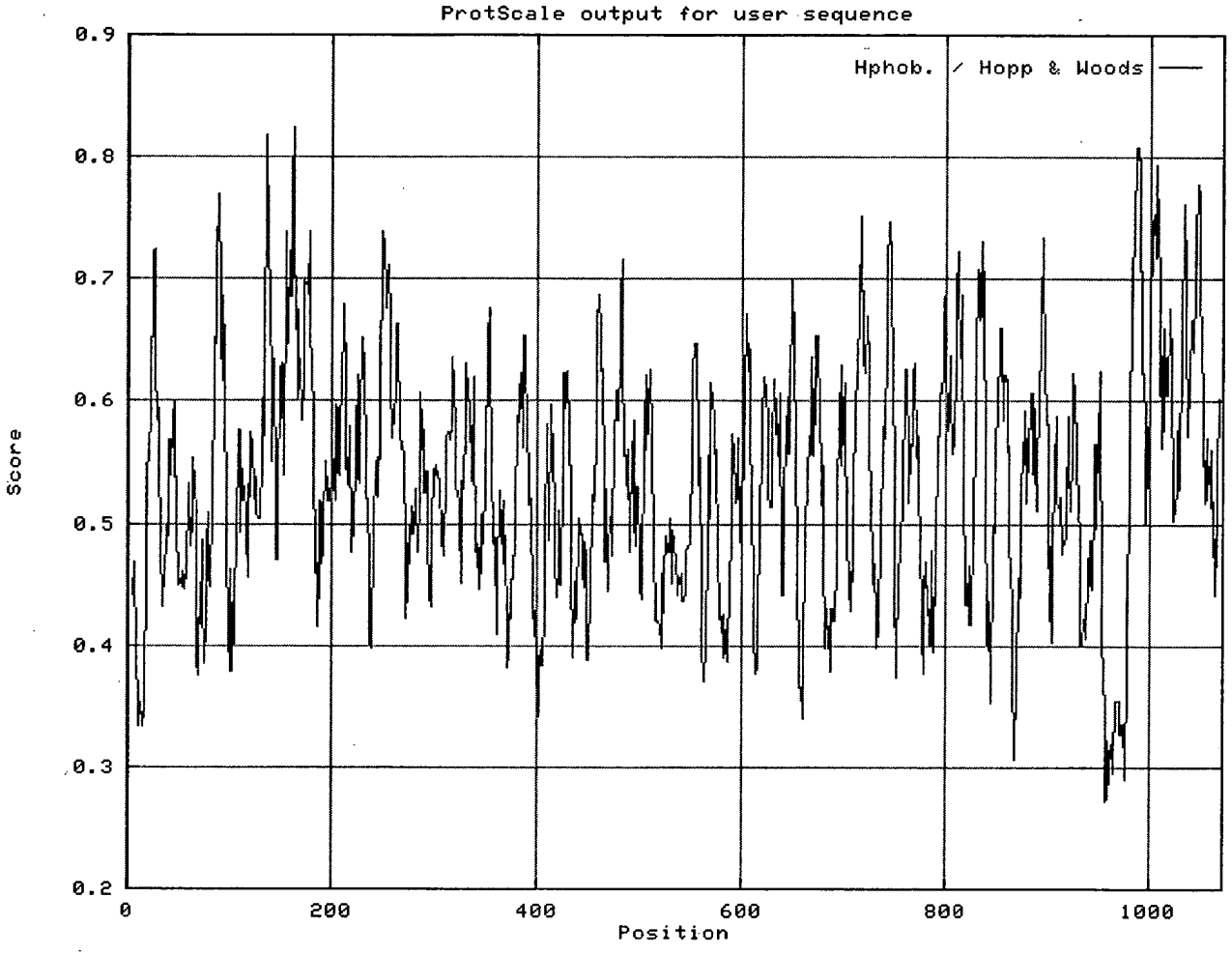


Figure 6: 254P1D6B variant 1
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

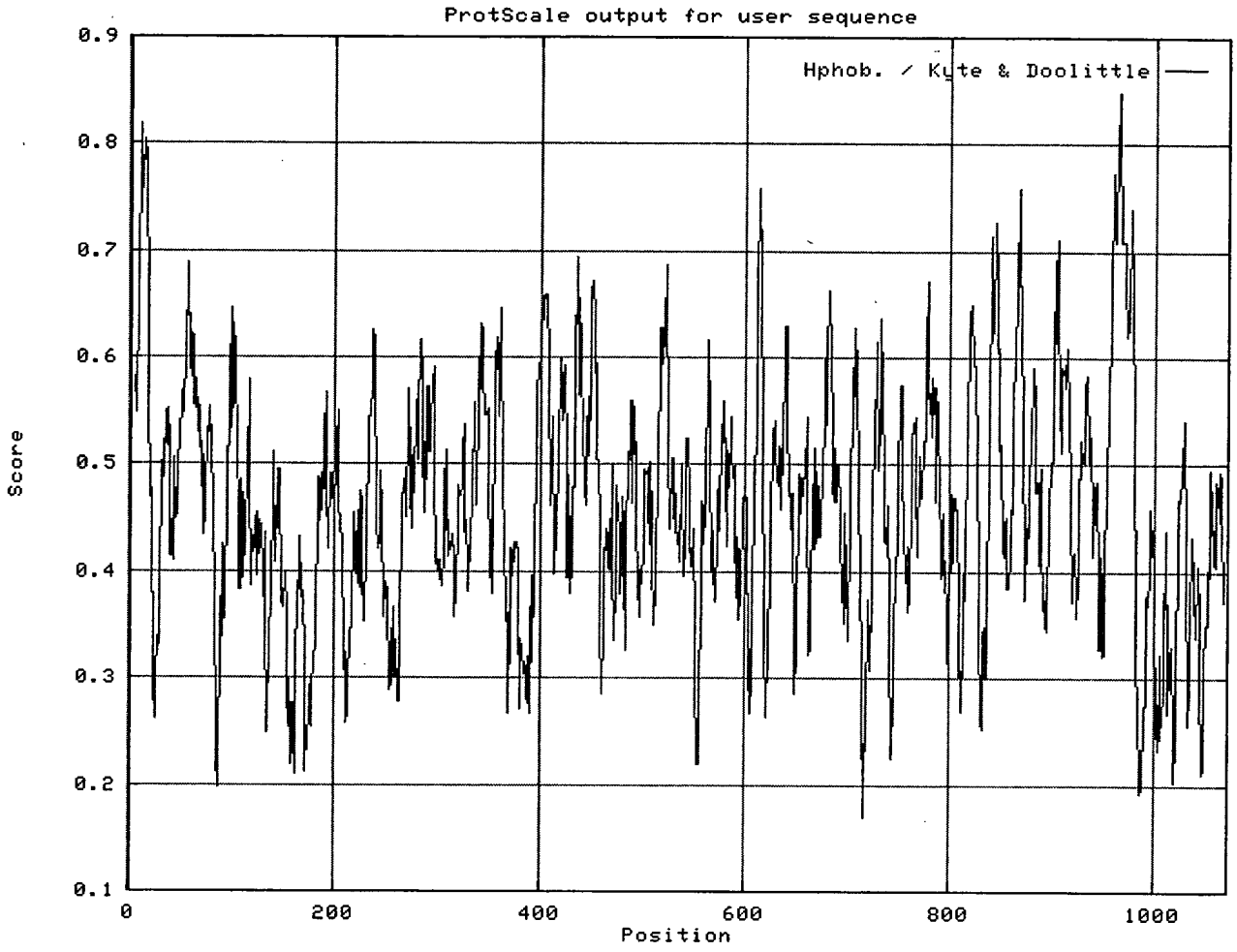


Figure 7: 254P1D6B variant 1
% Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

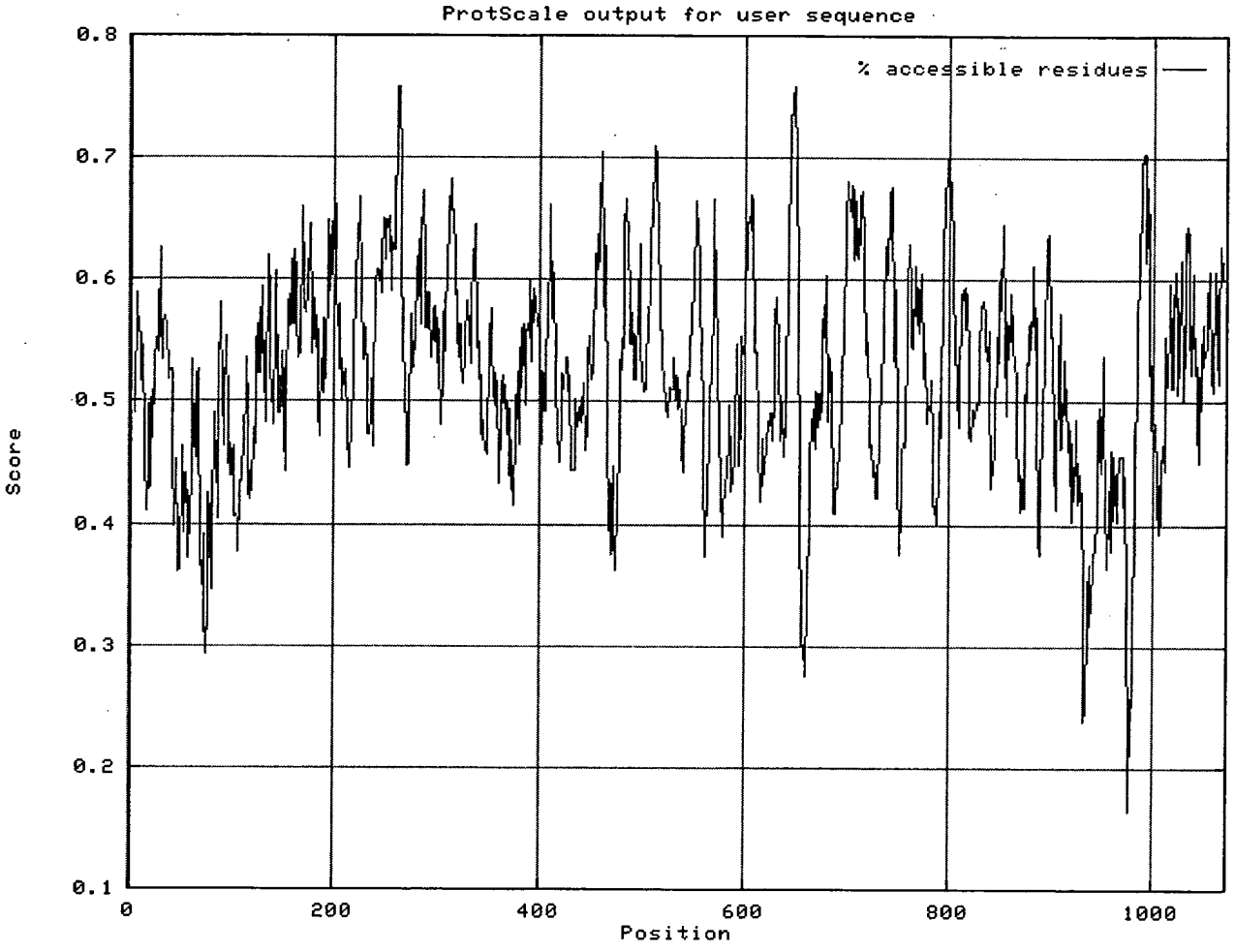


Figure 8: 254P1D6B variant 1
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

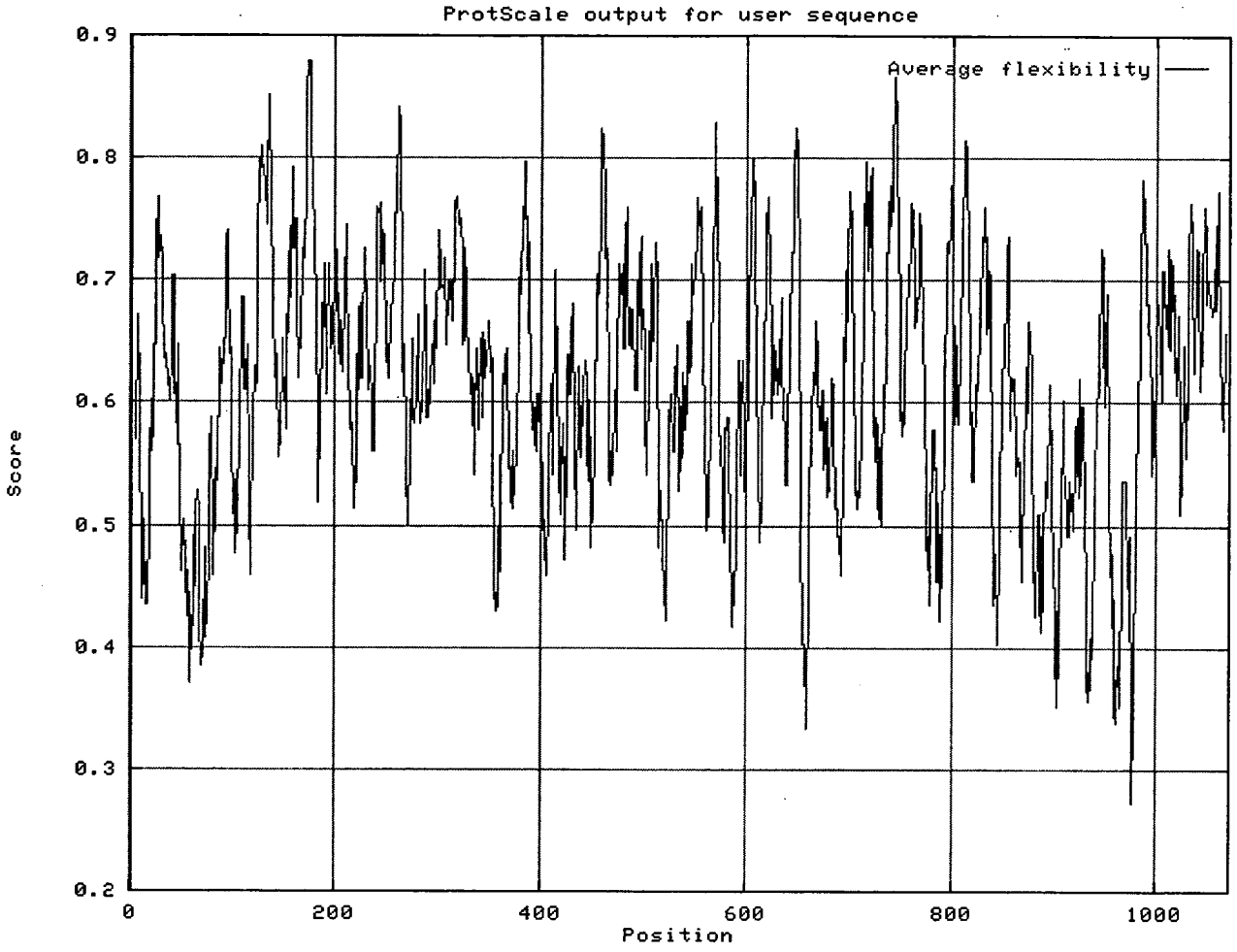


Figure 9: 254P1D6B variant 1
Beta-turn Profile
(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

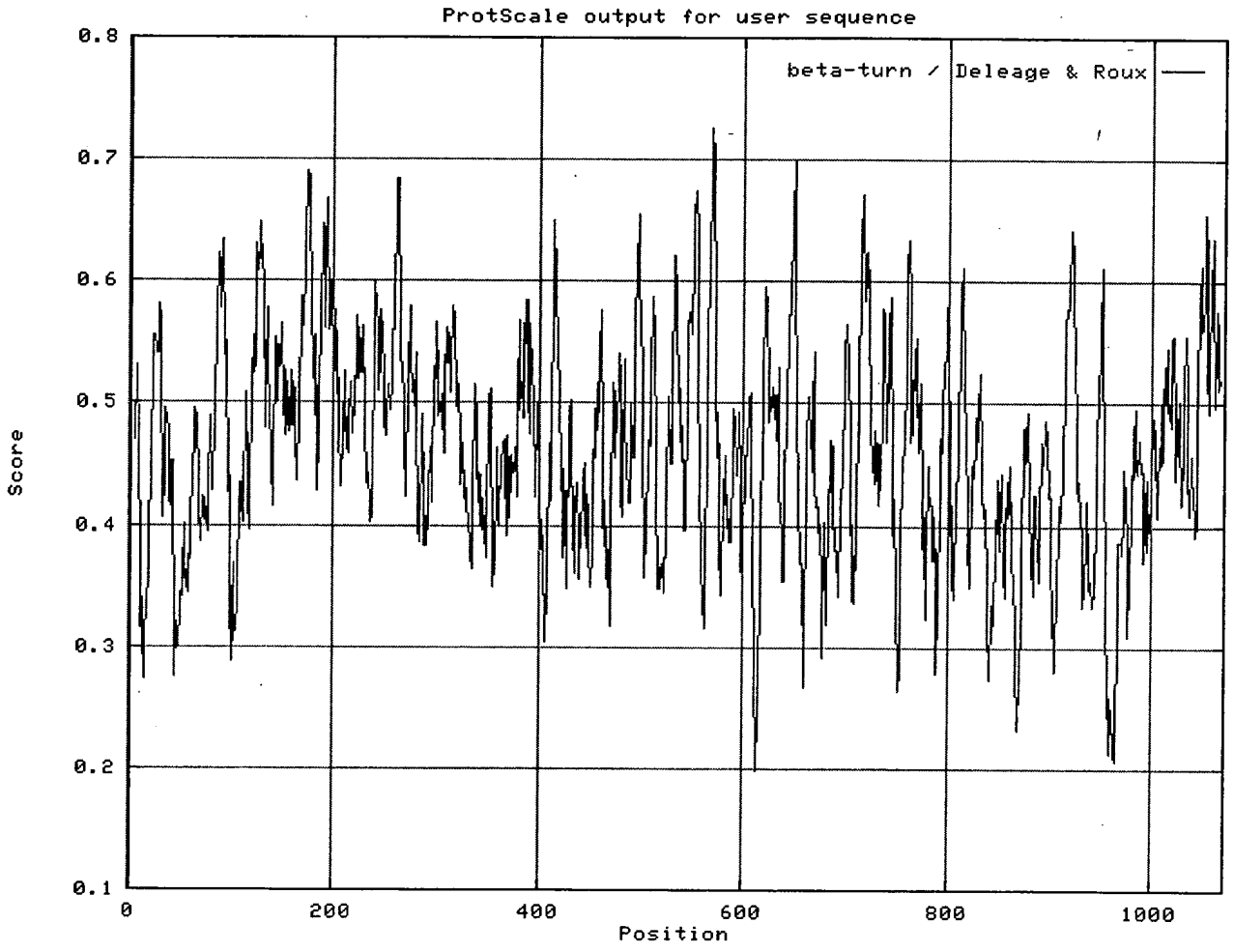
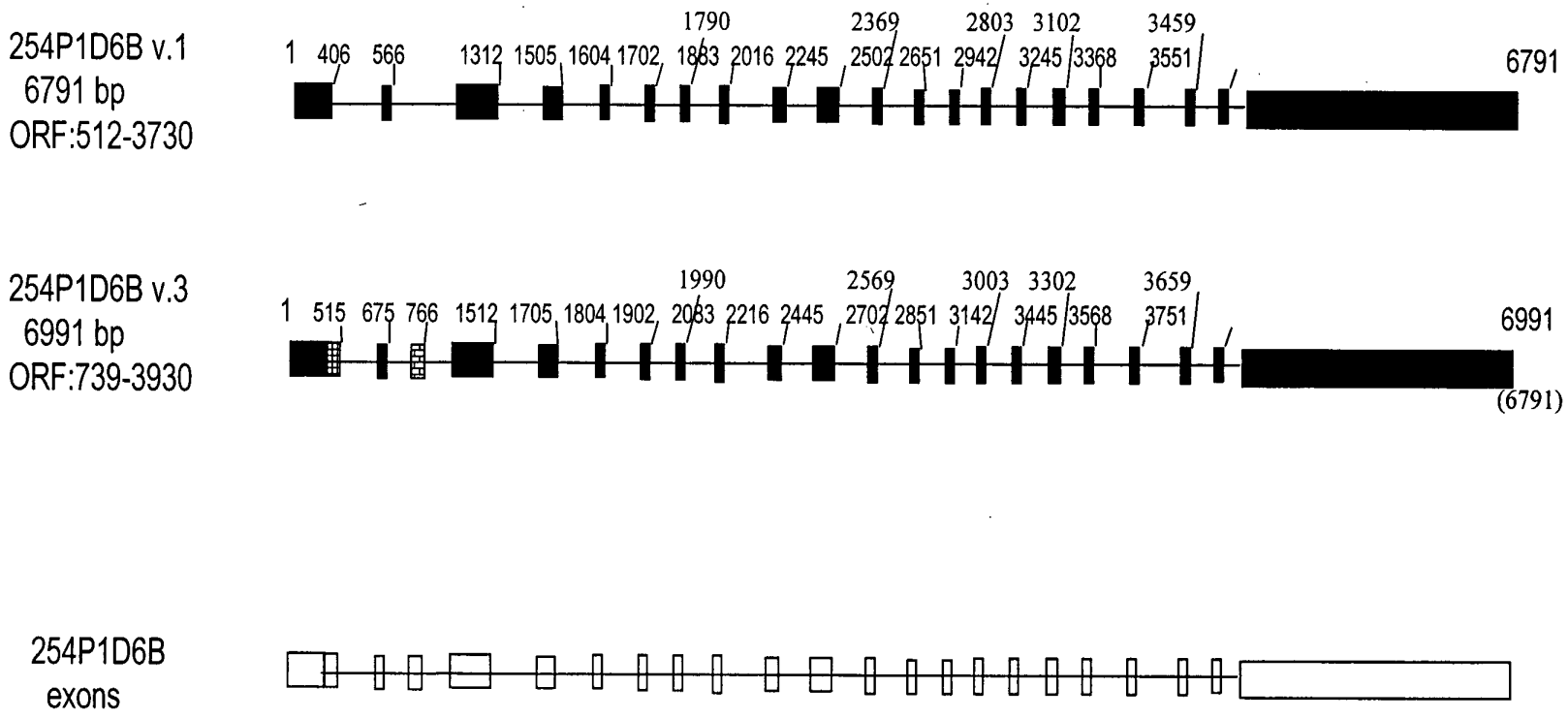


Figure 10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406
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1312
1505
1604
1702
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1883
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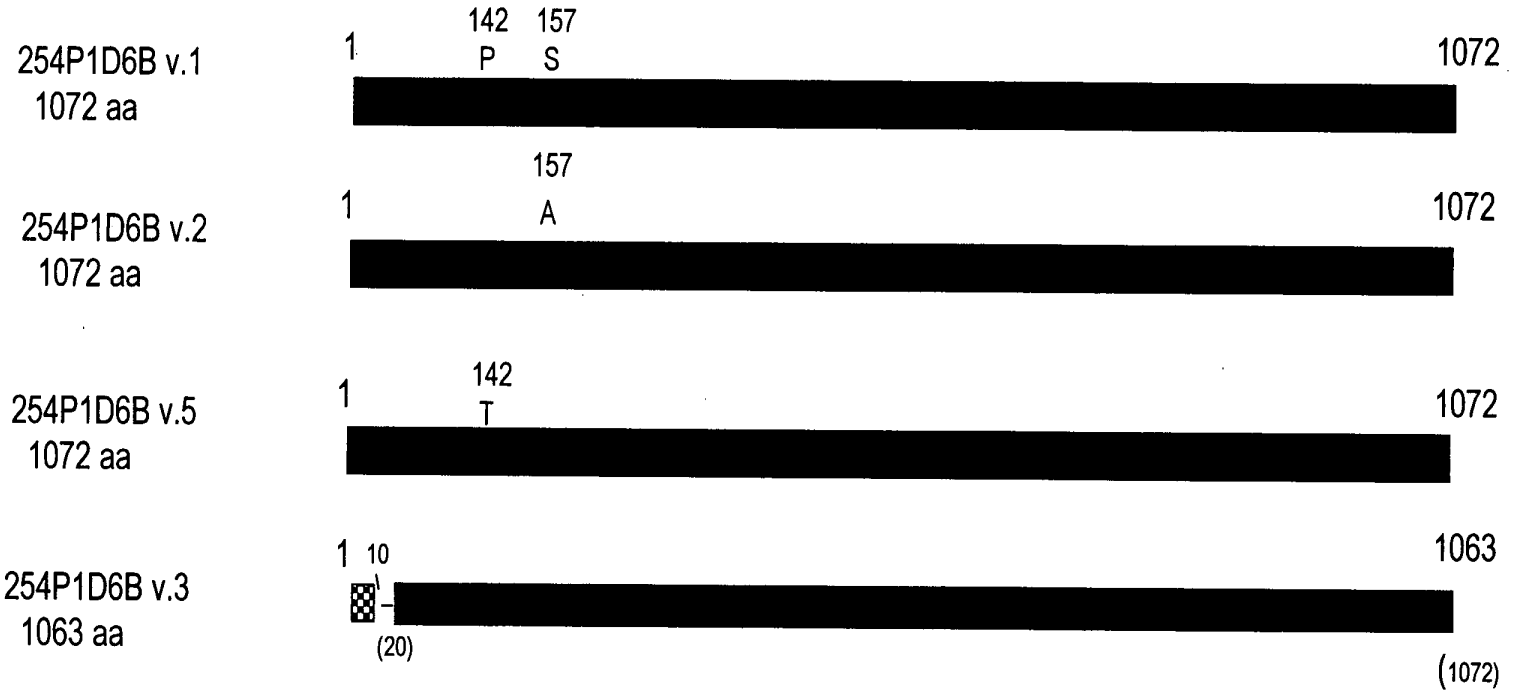
2245
2369
2502
2651
2803
2942
3102
3245
3368
3459
3551
6791
254P1D6B v.3
6991 bp
ORF:739-3930
1
515
675
766
1512
1705
1804
1902
1990
2083
2216
2445
2569
2702
2851
3003
3142
3302
3445
3568
3659
3751
6991
(6791)
254P1D6B
exons

Figure 11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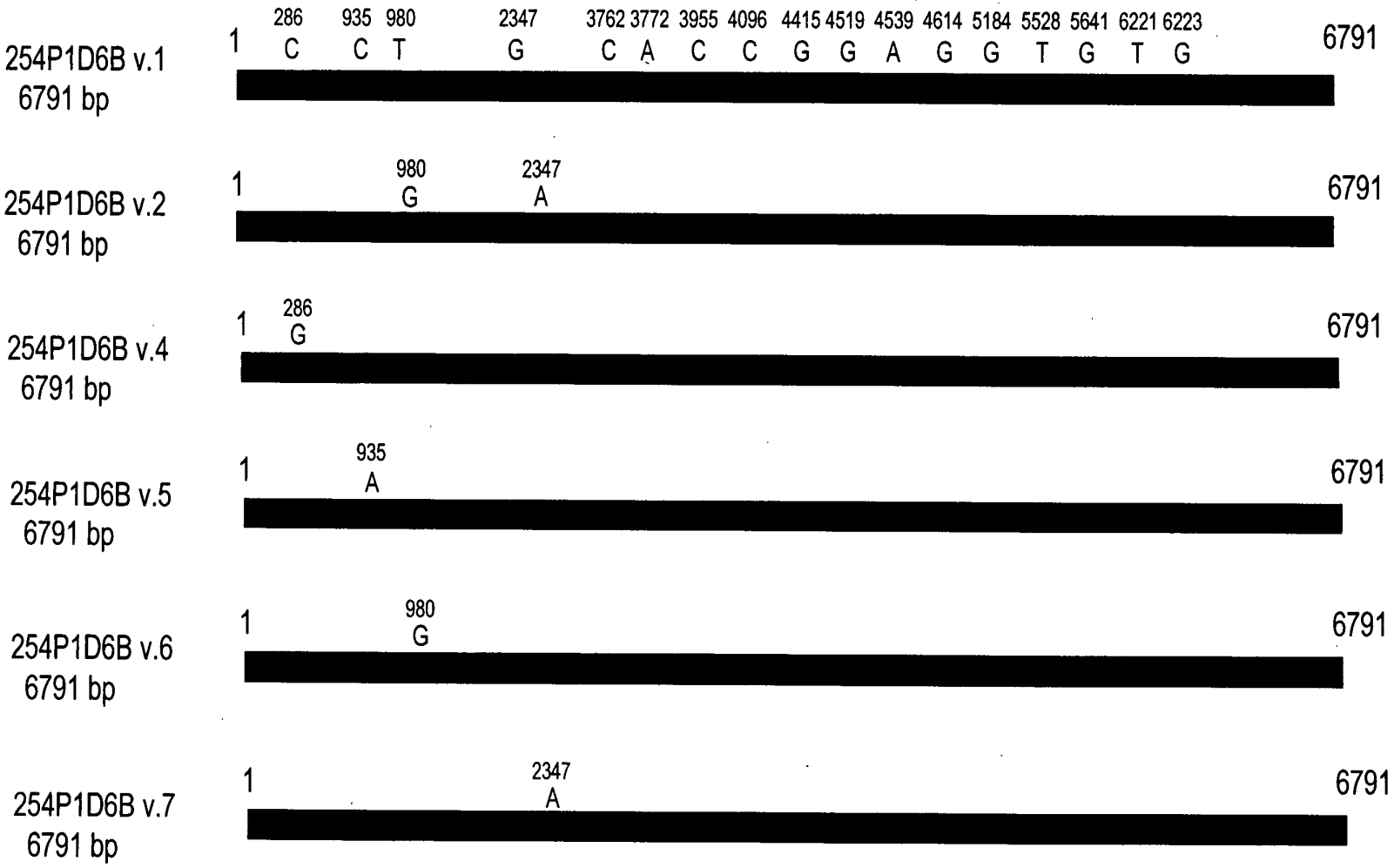
1072 aa
1
142
P
157
S
1072
254P1D6B v.2
1072 aa
1
157
A
1072
254P1D6B v.5
1072 aa
1
142
T
1072
254P1D6B v.3
1063 aa
1
10
(20)
1063
(1072)

Figure 12


254P1D6B v.1
6791 bp
1
286 C
935 C
980 T
2347 G
3762 C
3772 A
3955 C
4096 C
4415 G
4519 G
4539 A
4614 G
5184 G
5528 T
5641 G
6221 T
6223 G
6791
254P1D6B v.2
6791 bp
1
980 G
2347 A
6791
254P1D6B v.4
6791 bp
1
286 G
6791
254P1D6B v.5
6791 bp
1
935 A
6791
254P1D6B v.6
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1
980 G
6791
254P1D6B v.7
6791 bp
1
2347 A
6791

Figure 12 (con'd)

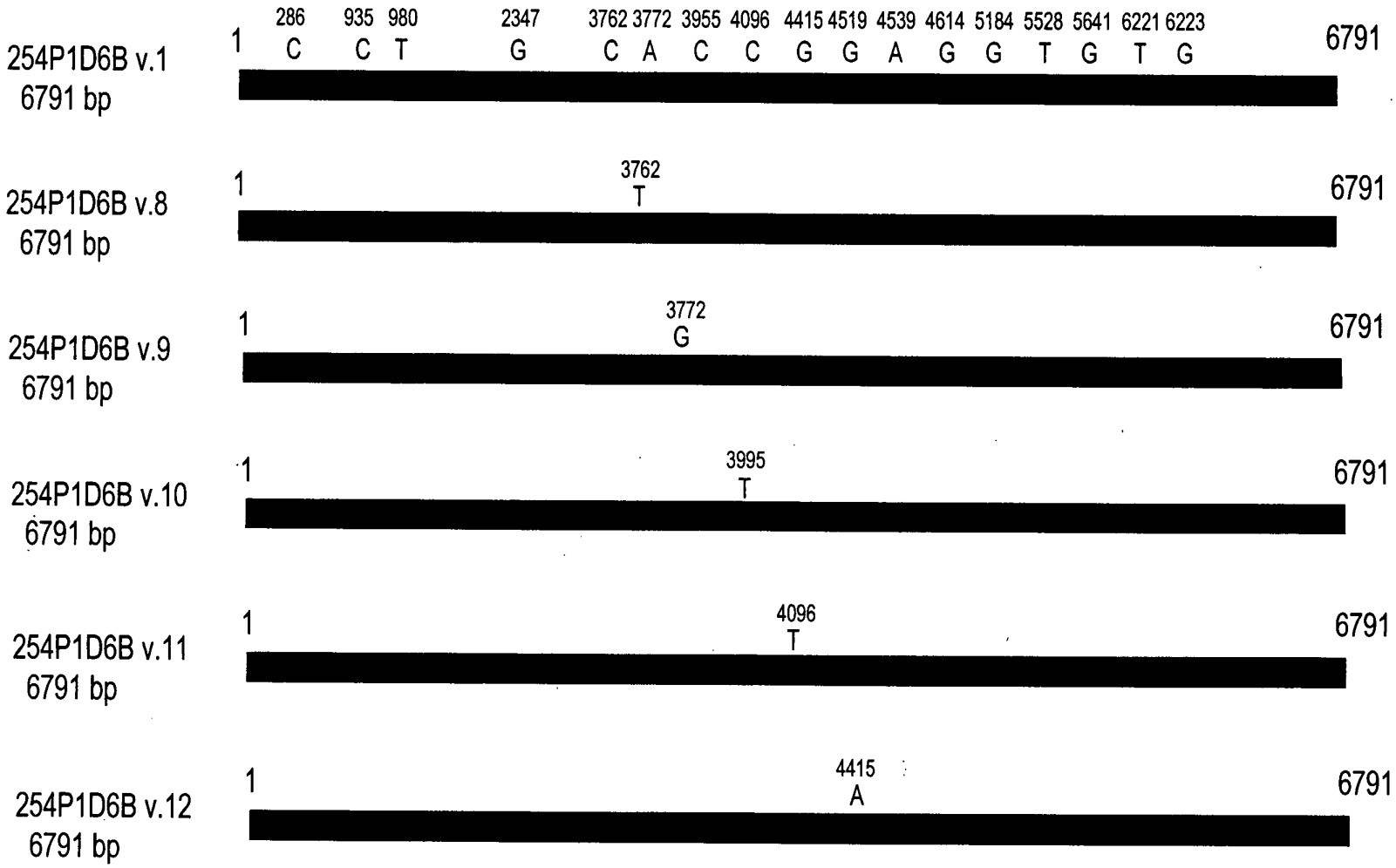


Figure 12 (con'd)

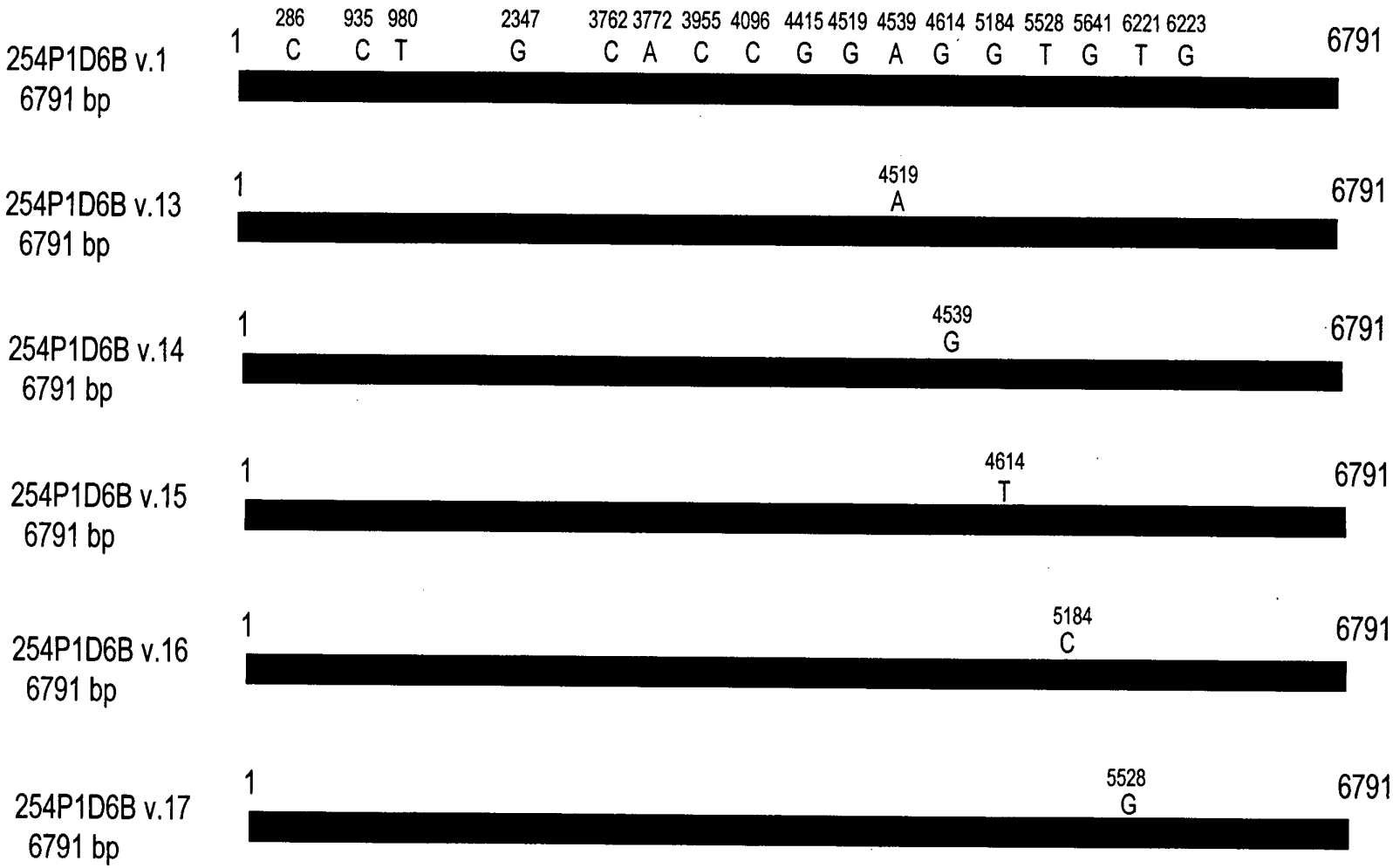


Figure 12 (con'd)

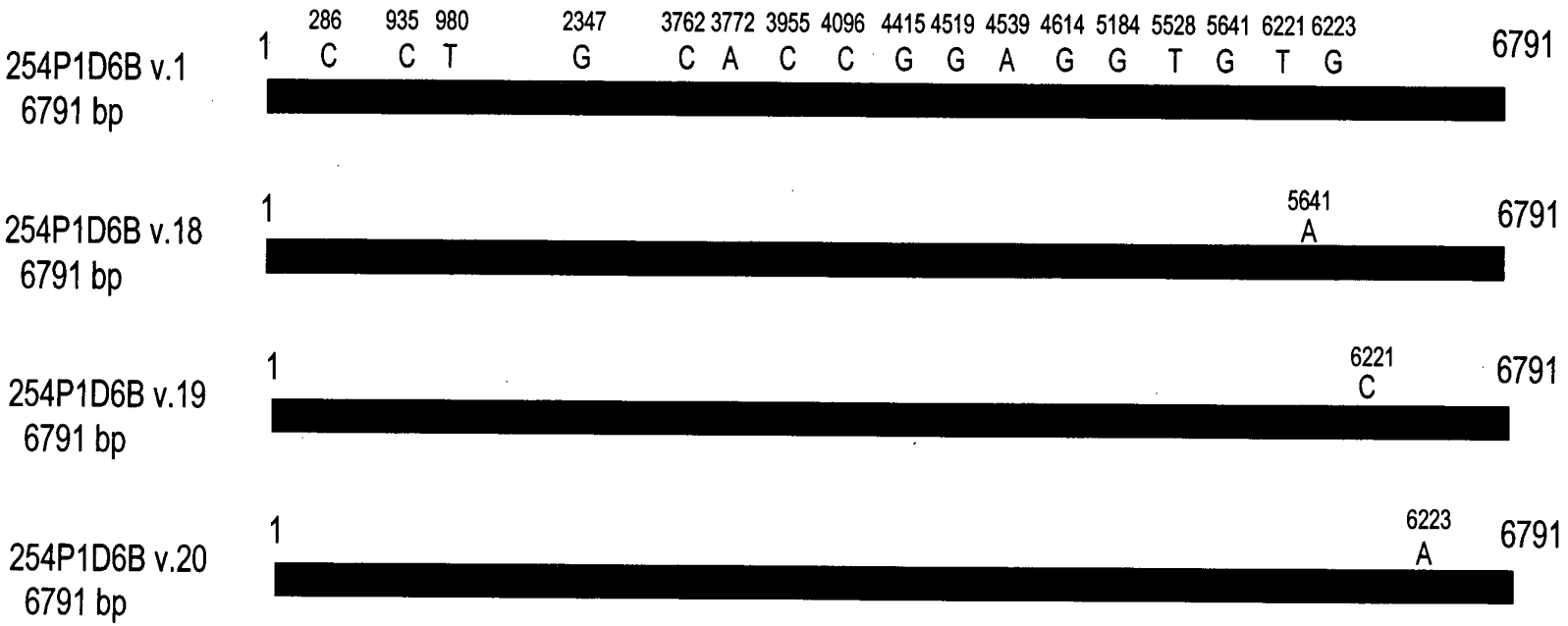


Figure 13: Secondary structure prediction of 254P1D6B variant 1

13A

```
          10        20        30        40        50        60        70        80
          |         |         |         |         |         |         |         |
MAPPTGVLSSLLLLVTIAGCARKQCSEGRTYSNAVISPNLETTRIMRVSHTFPVVDCTAACCDLSSCDLAWWFEGRCYLV
ccccccchhhhhhhhhhhhhchccccccccccceeeccccccceeeeeeeccccceeccccccccccccceeeeeccceeee
SCPHKENCEPKKMGPIRSYLTFVLRPVQRPAQLLDYGDMMLNRGSPSGIWGDSPEDIRKDLPFLGKDWGLEEMSEYSDDY
ecccccccccccccccceheheeeecchcccchhhcchhhccccccccccccchccccccccccccccchhhhhcchhh
RELEKDLLQPSGKQEPRGSAEYTDWGLLPGSEGAFNSSVGDSPAVPAETQQDPELHYLNESASTPAPKLPERSVLLPLPT
hhhhhhhccccccccccccccccccccccccccccccccccccccccccccccccccccceeeccccccccccccccceeccccc
TPSSGEVLEKEKASQLQEQSSNSSGKEVLMPSHSLPPASLELSSVTVEKSPVLTVTPGSTEHSIPTPPTSAAPSESTPSE
ccccchhhhhhhhchhhccccccccceeeeccccccccccceeeeeeeccccceeeeccccccccccccccccccccccccc
LPISPTTAPRTVKELTVSAGDNLIITLPDNEVELKAFVAPAPPVETTYNYEWNLISHPTDYQGEIKQGHKQTLNLSQLSV
ccccccccccccheeeeeccccceeeeeccccceeeeehccccccccccccceeeeeccccccccccchhhchhhheeheeecc
GLYVFKVTVSSENAFGEGFVNVTVKPARRVNLPPVAVVSPQLQELTLPLTSALIDGSQSTDDTEIVSYHWEEINGPFIEE
ceeeeeeeeeccccccccceeeeeeccccccccccccceeccchhcccccchheeccccccccceeeeeehhcccccceec
KTSVDSPVLRLSNLDPGNYSFRLTVTDSDGATNSTTAALIVNNAVDYPPVANAGPNHTITLPQNSITLNGNQSSDDHQIV
ccccccceeeeccccccccceeeeeeeccccccccchhhhhhhccccccccccccccceeeccccceeeccccccccccee
```

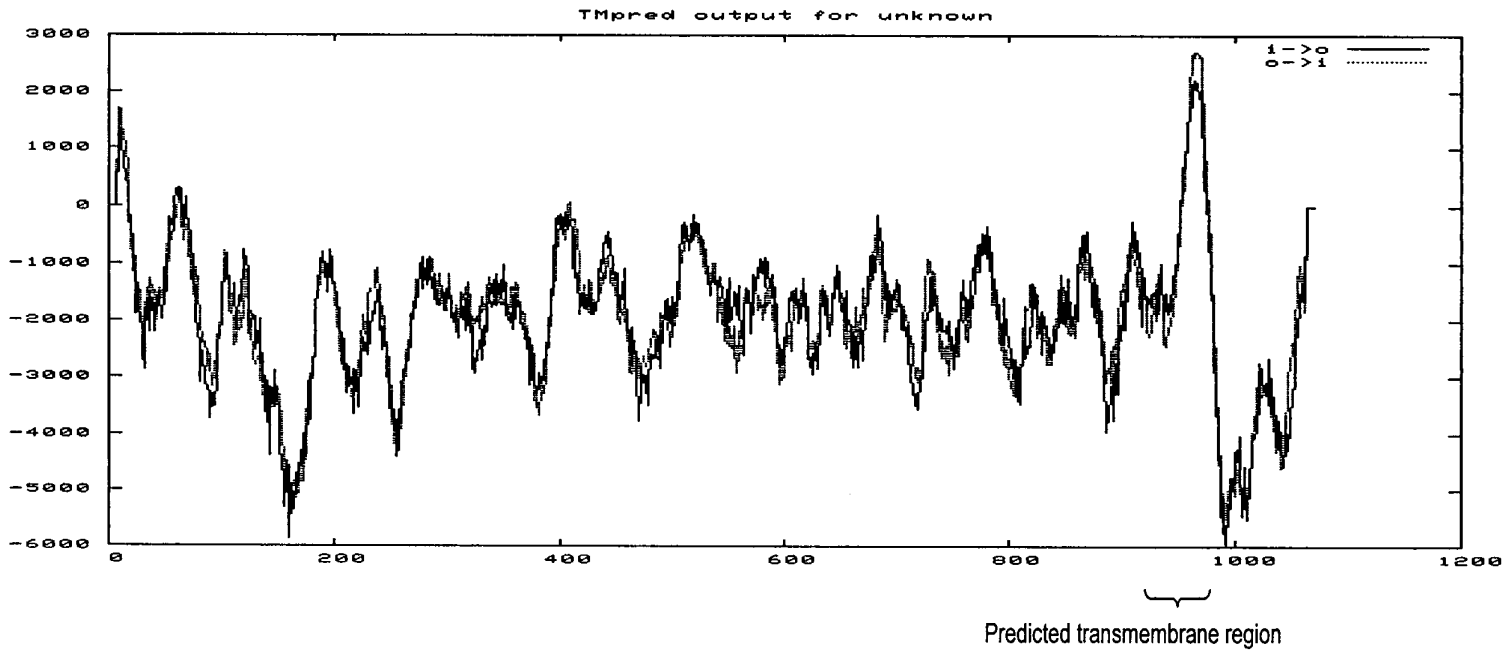
Alpha helix(h): 18.19%
Extended strand (e): 24.81%
Random coil(c): 57.00%

Secondary structure prediction of 254P1D6B variant 1 (continued)

```
        570       580       590       600       610       620       630       640
         |         |         |         |         |         |         |         |
LYEWSLGPGSEGKHVVMQGVQTPYLHLSAMQEGDYTFQLKVTDSSRQQSTAVVTVIVQPENNRPPVAVAGPDKELIFPVE
eeeeccccccccceeeeeccccccheeeehccccccceeeeeeccccccccceeeeeeeeeccccccceeeccccceeeeeec
SATLDGSSSSDDHGIVFYHWEHVRGPSAVEMENIDKAIATVTGLQVGTYHFRLTVKDQQGLSSTSTLTVAVKKENNSPPR
ccccccccccccceeeeeeeccccccccchhhhhhhhhhhhhcccceeccceeeeeeeeccccccccceeeeeeeccccccc
ARAGGRHVLVLPNNSITLDGSRSTDDQRIVSYLWIRDGQSPAAGDVIDGSDHSVALQLTNLVEGVYTFHLRVTDSQGASD
ccccccceeeeeccccceeeccccccccccceeeeeeeeccccccccccccccccccccheeehhhhhhhcheeeeeeeccccccc
TDTATVEVQPDPRKSGLVELTLQVGVGQLTEQRKDTLVRQLAVLLNVLDSDIKVQKIRAHSDLSTVIVFYVQSRPPFKVL
ccccceeeeccccccccheeeeeeeccccccchhhhhhhhhhhhhhhhhhcccchhhhehhcccccceeeeeeeccccccchhh
KAAEVARNLHMRLSKEKADFLLFKVLRVDTAGCLLKCSGHGHCDPLTKRCICSHLWMENLIQRYIWDGESNCEWSIFYVT
hhhhhhhhhhhhhhhhhhhhhhheheeeccccceeeeccccccccccchhhhhhhhhhhhhhhhhheccccccchhhhhhhh
VLAFTLIVLTGGFTWLCICCCKRQKRTKIRKKTKYTILDNMDEQERMELRPKYGIKHRSTEHNSSLMVSESEFDSDQDTI
hheeeeeeeccccceeeeeeeccccchcchccccccceeeeccccchhhhhhcccccceeeeccccccceeeeeccccccchhhh
FSREKMERGNPKVSMNGSIRNGASFSYCSKDR
ehhhhhhccccceeccccccccccceeeccccc
```

Alpha helix(h): 18.19%
Extended strand (e): 24.81%
Random coil(c): 57.00%

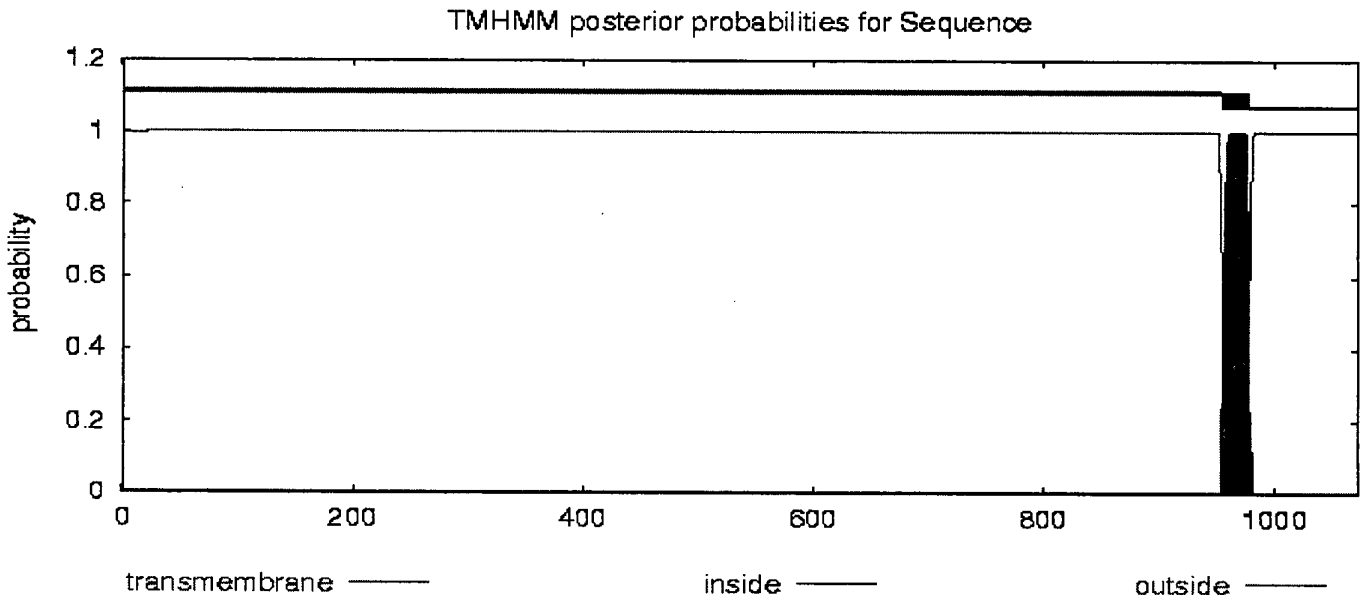
Figure: 13B **Transmembrane prediction for 254P1D6B variant 1**



1 transmembrane domain predicted

Figure: 13C

Transmembrane prediction for 254P1D6B variant 1



1 transmembrane domain predicted

Figure 14A 254P1D6B Expression by RT-PCR

M = Marker

1) Vital Pool 1
   (Kidney, Liver, Lung)
2) Vital Pool 2
   (Colon, Pancreas, Stomach)
3) Normal Lung
4) Lung Cancer Pool
5) Ovary Cancer Pool
5) Pancreas cancer Pool

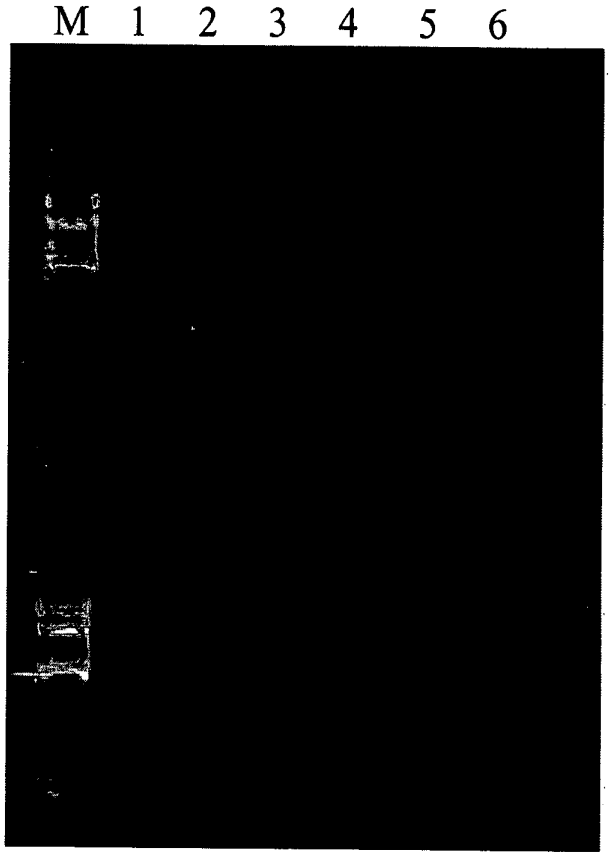


Figure 14B Expression of 254P1D6B in Normal Human Tissues and Ovarian Cancer Patient Specimens

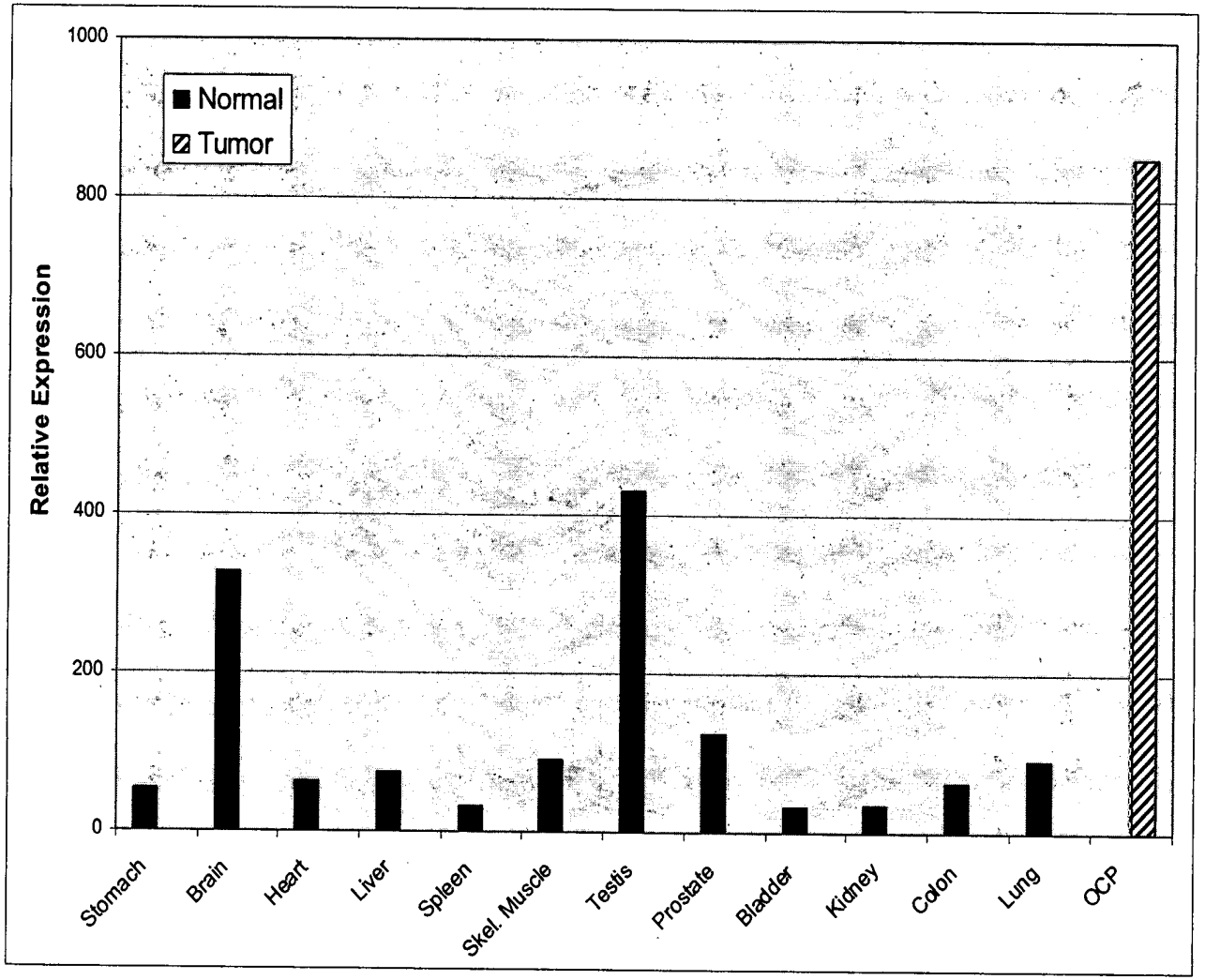
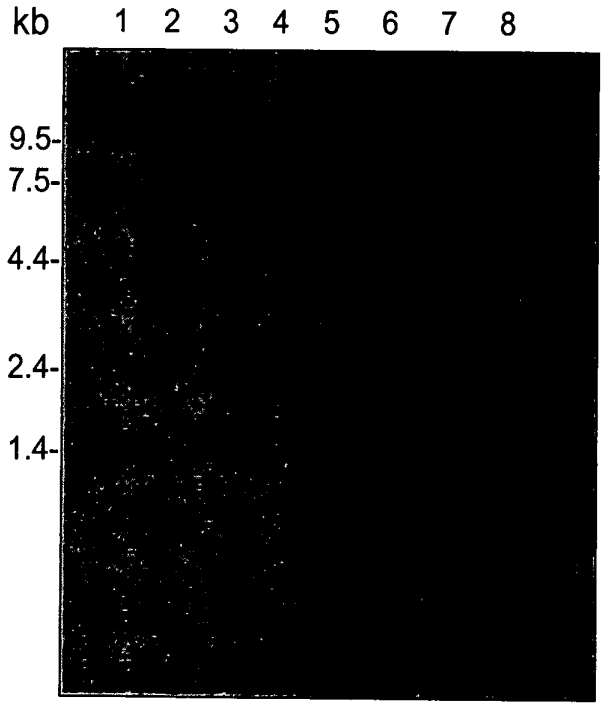
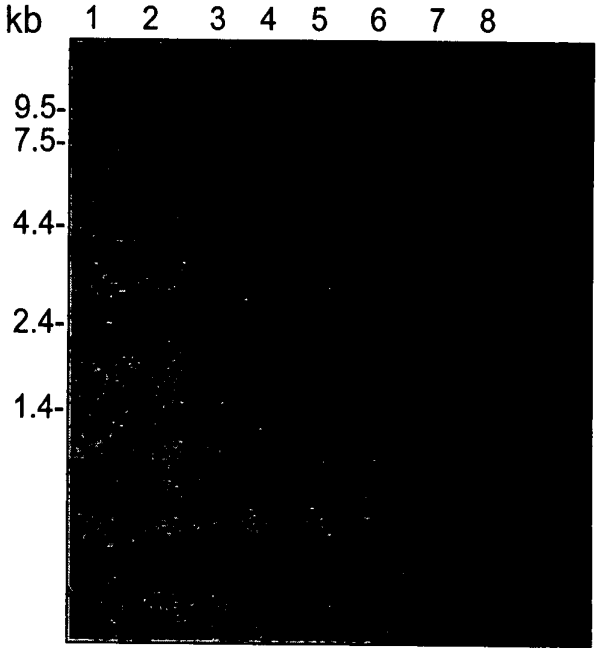


Figure 15 Expression of 254P1D6B in Normal Tissues



1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas



1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Uterus
6. Small Intestine
7. Colon
8. Leukocytes

Figure 16 Expression of 254P1D6B in Lung Cancer Patient Specimens

Panel#	Pathology	Grade	Expression
1	Normal		
2	A427 Cell line		
3	Adeno	3	
4	Adeno	I	
5	Adeno	IB	
6	Adeno	IB	
7	Adeno	IIIA	
8	Adeno	IIIA	
9	Adeno	Mod Diff	
10	Adeno	Mod Diff	
11	Adeno		
12	Bronchioalv.	IA	
13	Large Cell	I	
14	Large Cell	IIB	
15	Large Cell	IIIA	
16	Large Cell	IV	
17	Papillary	I	
18	Papillary	IB	
19	Papillary	IV	
20	Small Cell	I	
21	Small Cell	I	
22	Small Cell	I	
23	Small Cell	IIB	
24	Squamous	IB	
25	Squamous	IB	
26	Squamous	IB	
27	Squamous	IIB	
28	Squamous	IIB	
29	Squamous	IIIA	
30	Squamous	IIIA	
31	Squamous		
32	Squamous		
33	Squamous		

	No Expression
	Low Expression
	High expression

Figure 17: Expression of 254P1D6b in 293T cells

Figure 17A

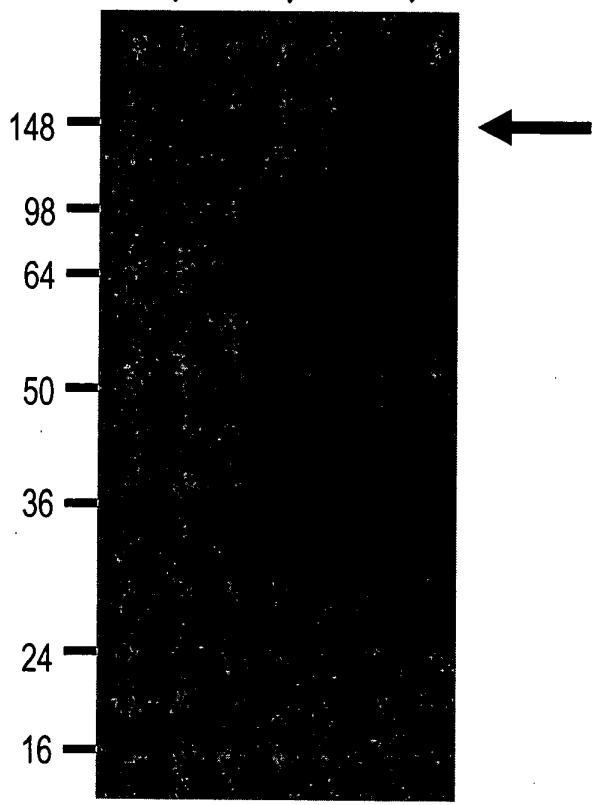


Figure 17B